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- (A) Non-reducing saccharide-forming enzyme, DNA encoding it, and their preparations and uses.
- (57) A DNA encoding an enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from amylaceous saccharides having a degree of glucose polymerization of 3 or higher, enables an industrial-scale production of a recombinant enzyme with such enzyme activity. Non-reducing saccharides obtainable by the recombinant enzyme can be used in a variety of food products, cosmetics, pharmaceuticals and feeds because of their substantial non-reducibility, mild and high-quality sweetness, adequate viscosity, and moisture-retaining ability.

The present invention relates to a novel DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and a recombinant DNA and enzyme containing the DNA as well as to a transformant. The present invention further relates to preparations and uses thereof.

Trehalose is a disaccharide which consists of 2 glucose molecules that are linked together with their reducing groups, and, naturally, it is present in fungi, algae, insects, etc., in an extremely small quantity. Having no reducing residue within the molecule, trehalose does not cause an unsatisfactory browning reaction even when heated in the presence of amino acids or the like, and because of this it can sweeten food products without fear of causing unsatisfiable coloration and deterioration. Trehalose, however, is far from being readily prepared in a desired amount by conventional production methods, and, actually, it has not scarcely been used for sweetening food products.

Conventional production methods are roughly classified into 2 groups, i.e. the one using cells of microorganisms and the other employing a multi-enzymatic system wherein enzymes are allowed to act on saccharides. The former, as disclosed in Japanese Patent Laid-Open No.154,485/75, is a method comprising growing microorganisms such as bacteria and yeasts in nutrient culture media, and collecting trehalose from the proliferated cells in the resultant cultures. The latter, as disclosed in Japanese Patent Laid-Open No.216,695/83, is a method comprising providing maltose as a substrate, allowing a multi-enzymatic system using maltose-and trehalose-phosphorylases to act on maltose, and recovering the formed trehalose from the reaction system. Although the former facilitates to grow microorganisms with a relative easiness, it requires sequential complicated steps for collecting trehalose from the microorganisms containing only 15 w/w % trehalose, on a dry solid basis (d.s.b.). While the latter enables to separate trehalose with a relative easiness, but it is theoretically difficult to increase the trehalose yield by allowing enzymes to act on substrates at a considerably-high concentration because the enzymatic reaction in itself is an equilibrium reaction of 2 different types of enzymes and the equilibrium point constantly inclines to the side of forming glucose phosphate.

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In view of the foregoing, the present inventors energetically screened enzymes which form saccharides having trehalose structure from amylaceous saccharides, and found that microorganisms such as those of the spices *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 produce a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Before or after this finding, it was revealed that such a non-reducing saccharide is almost quantitatively hydrolyzed into trehalose and glucose and/or maltooligosaccharides by another enzyme produced by the same microorganisms as mentioned above. Since the combination use of the enzymes enables to form a desired amount of trehalose with a relative easiness, the aforementioned objects relating to trehalose would be completely overcome. Insufficient producibility of the novel enzyme by such a microorganism results in a drawback, i.e. a relatively-large scale culture thereof is inevitable to industrially produce trehalose and/or non-reducing saccharides having trehalose structure as an end unit.

Recombinant DNA technology has made a remarkable progress in recent years. At present, even an enzyme whose total amino acid sequence has not been revealed can be readily prepared in a desired amount, if a gene encoding the enzyme was once isolated and the base sequence was decoded, by preparing a recombinant DNA which contains a DNA encoding the enzyme, introducing the recombinant DNA into microorganisms or cells of plants and animals, and culturing the resultant transformants. Under the background, urgently required are to find a gene encoding the enzyme and to reveal a base sequence thereof.

It is an aim of the present invention to provide a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

It is a further aim of the present invention to provide a recombinant DNA which contains the DNA and a self-replicable vector.

It is yet another aim of the present invention to provide a recombinant enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, by means of recombinant DNA technology.

It is another alm of the present invention to provide a transformant obtainable by introducing the recombinant DNA into a suitable host.

It is a further aim of the present invention to provide a preparation of the recombinant enzyme.

It is yet another aim of the present invention to provide a method to converting ducing amylaceous saccharides by using the recombinant enzyme.

The pr sent invention provides a DNA encoding an enzyme which forms non-r ducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a replicable recombinant DNA which contains a self-r plicable vec-

tor and a DNA which encodes a non-reducing saccharide-forming enzyme.

The present invention further provides a recombinant enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a transformant into which a replicable recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a process for producing a recombinant enzyme, which contains a step of culturing a transformant capable of forming the recombinant enzyme, and collecting the enzyme from the resultant culture.

The present invention further provides a method for converting reducing amylaceous saccharides, which contains a step of allowing the recombinant enzyme to act on reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher to form from them non-reducing saccharides having trehalose structure as an end unit.

The invention will now be described in further detail, by way of example only, with reference to the accompanying drawings, in which:

- FIG. 1 shows the optimum temperature of enzyme M-11.
- FIG. 2 shows the optimum temperature of enzyme Q36.
- FIG. 3 shows the optimum pH of enzyme M-11.
- FIG. 4 shows the optimum pH of enzyme Q36.
- FIG. 5 shows the thermal stability of enzyme M-11.
- FIG. 6 shows the thermal stability of enzyme Q36.
- FIG. 7 shows the pH stability of enzyme M-11.
- FIG. 8 shows the pH stability of enzyme Q36.
- FIG. 9 is a restriction map of the recombinant DNA pBMT7 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme M-11.
- FIG. 10 is a restriction map of the recombinant DNA pBQT13 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme Q36.

The DNA according to the present invention exerts the production of the non-reducing saccharide-forming enzyme encoded by the DNA in a manner that the DNA is inserted into an appropriate self-replicable vector to form a replicable recombinant DNA, followed by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but readily replicable, to form a transformant.

Although the recombinant DNA per se does not produce the enzyme, the production of the enzyme encoded by the DNA is induced by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but replicable with a relative easiness, to form a transformant, and culturing the transformant to produce the enzyme.

The transformant according to the present invention produces the enzyme when cultured.

The recombinant enzyme according to the present invention acts on reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher to form non-reducing saccharides having trehalose structure as an end unit.

The culture of the transformant according to the present invention yields a desired amount of the enzyme with a relative easiness.

The conversion method according to the present invention converts reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher into non-reducing saccharides having trehalose structure as an end unit.

The present invention was made based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. The enzyme can be obtained from cultures of microorganisms of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 (the enzymes from *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 are respectively designated as "enzyme M-11" and "enzyme Q36" hereinafter), and the present inventors isolated the enzyme by the combination use of conventional purification methods using column chromatography mainly, and examined the properties and features to reveal the reality, i.e. a polypeptide having the following physicochemical properties:

(1) Action

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Forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degre of glucose polymerization of 3 or higher;

(2) Molecular w ight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide g | lelectrophoresis (SDS-PAGE);

11.

25... (3) Isoelectric point

: About 3.6-4.6 on isoelectrophoresis; 🤼 😭

(4) Optimum temperature

Exhibiting an optimum temperature of around 35-40°C when incubated at pH 7.0 for 60 min;

(5) Optimum pH 1121

Exhibiting an optimum pH of around 6.4-7.2 when incubated at 40°C for 60 min;

(6) Thermal stability

Stable up to a temperature of around 35-40°C when incubated at pH 7.0 for 60 min; and

(7) pH Stability 2 has a 2 same to controller

Stable up to a pH of around 5.5-11.0 when incubated at 25°C for 16 hours.

The experiments, which were conducted to reveal the aforesaid physicochemical properties, are explained in the below:

#### 15 Experiment 1

Preparation of purified enzyme

#### Experiment 1-1

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#### Preparation of enzyme derived from Rhizobium sp. M-11

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) containing 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate, and 0.1 w/v % potassium dihydrogen phosphate, and the flasks were autoclaved at 120°C for 20 min to effect sterilization. After cooling the flasks a seed culture of *Rhizobium* sp. M-11 was inoculated into each liquid culture medium in each flask, followed by the incubation at 27°C for 24 hours under rotary-shaking conditions. Twenty L of a fresh preparation of the same liquid culture medium was put in a 30-L jar fermentor and sterilized, followed by inoculating one v/v % of the culture obtained in the above into the sterilized liquid culture medium in the jar fermentor, and incubating it at a pH of 6-8 and 30°C for 24 hours under aeration and agitation conditions.

Thereafter, about 18 L of the resultant culture was subjected to an ultra-high pressure cell disrupting apparatus to disrupt cells, and the resultant suspension was centrifuged to obtain a supernatant, and to about 16 L of which was added ammonium sulfate to give a 20 w/v % saturation, allowed to stand at 4°C for one hour, and centrifuged to remove sediment. To the resultant supernatant was added ammonium sulfate to give a 60 w/v % saturation, allowed to stand at 4°C for 24 hours, and centrifuged to collect sediment which was then dissolved in a minimum amount of 10 mM phosphate buffer (pH 7.0). The resultant solution was dialyzed against 10 mM phosphate buffer (pH 7.0) for 24 hours, and centrifuged to remove insoluble substances. The supernatant thus obtained was fed to a column packed with "DEAE-TOYOPEARL®", a product for ion-exchange chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM phosphate buffer (pH 7.0), followed by feeding to the column a linear gradient buffer of sodium chloride ranging from 0 M to 0.5 M in 10 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, dialyzed for 10 hours against 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, and centrifuged to remove insoluble substances. Thereafter, the resultant supernatant was fed to a column, which had been packed with "BUTYL TOYOPEARL®", a gel for hydrophobic column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, and equilibrated with 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, followed by feeding to the column a linear gradient buffer of ammonium sulfate ranging from 2 M to 0 M in 50 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, fed to a column packed with "TOYOPEARL® HW-55", a product for gel filtration column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 50 mM phosphate buffer (pH 7.0), followed by feeding to the column 50 mM phosphate buffer (pH 7.0) and collecting fractions containing the objective enzyme. The enzyme thus obtained had a specific activity of about 195 units/mg protein, and the yield was about 220 units per L of the culture.

Throughout the specification the enzyme activity is expressed by the value on the following assay: Place 4 ml of 50 mM phosphate buffer (pH 7.0) containing 1.25 w/v % maltopentaose in a test tube, add one ml of an enzyme solution to the tube, and incubate the resultant solution at 40°C for 60 min to effect enzymatic reaction. There after, heat the resultant reaction mixture at 100°C for 10 min to suspend the enzymatic reaction. Dilute the resultant reaction mixture with distilled water by 10 times, and assay the reducing activity

on the Somogyi-Nelson's method. One unit activity of the enzyme is defined as the amount of enzyme which reduces the reducing power corresponding to one  $\mu$ mol maltopentaose per min under the same conditions as described above.

# Experiment 1-2

#### Purification of enzyme Q36

Similarly as in Experiment 1-1, a seed culture of *Arthrobacter* sp.Q36 was cultured, and the resultant culture was treated to obtain a purified enzyme Q36 having a specific activity of about 200 units/mg protein in a yield of about 295 units per L of the culture.

#### **Experiment 2**

# Physicochemical property of enzyme

#### Experiment 2-1

#### Action

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To 50 mM phosphate buffer (pH 7.0) containing 20 w/v % of glucose, maltose, maltotriose, maltotetraose, maltopentaose, maltohexaose or maltoheptaose as a substrate was added 2 units/g substrate, d.s.b., of the purified enzyme M-11 or enzyme Q36 obtained in Experiment 1, and the mixture was enzymatically reacted at 40°C for 48 hours. The reaction mixture was desalted in usual manner, fed to "WB-T-330", a column for high-performance liquid chromatography (HPLC) commercialized by Tosoh Corporation, Tokyo, Japan, followed by feeding to the column distilled water at a flow rate of 0.5 ml/min at ambient temperature to separate saccharides contained in the reaction mixture while monitoring the saccharide concentration of the eluate with "MODEL RI-8012", a differential refractometer commercialized by Wako Pure Chemical Industries, Ltd., Tokyo, Japan. The saccharide composition of the reaction mixture was given in Table 1 or 2. In the table, the symbols "P1" to "P5" were named for the formed saccharides in the order from the smallest one to the largest one in terms of their degrees of glucose polymerization.

Table '

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Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Glucose	Glucose	33.4	100.0
Maltose	Maltose	28.5	100.0
Maltotriose	P1	23.3	35.0
	+ Maltotriose	25.9	65.0
Maltotetraose	P2	21.6	85.6
	+ Maltotetraose	24.1	14.4
Maltopentaose	Р3	19.7	92.7
	+ Maltopentaose	22.6	7.3
Maltohexaose	p4	18.7	93.5
	+ Maltohexaose	21.4	6.5
Maltoheptaose	P5	17.8	93.4
	+ Maltoheptaose	21.0	6.7

Table 2

Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Glucose	Glucose	33.4	100.0
Maltose	Maltose	28.5	100.0
Maltotriose	P1 + Maltotriose	23.3 25.9	35.5 64.5
Maltotetraose	P2 + Maltotetraose	21.6 24.1	85.8 14.2

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	Saccharide in reaction mixture	Elution time (min)	Composition (%)
Maltopentaose	P3 + Maltopentaose	19.7 22.6	92.9
Maltohexaose	P4 + Maltohexaose	18.7 21.4	93.2
Maltoheptaose	P5 + Maltoheptaose	17.8 21.0	93.1 6.9

As is evident from the results in Table 1 and 2, the enzymes M-11 and Q36 newly formed saccharides from reducing saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose, but not from those having a degree of glucose polymerization less than 3 such as glucose and maltose. In the enzymatic reaction, the newly formed saccharides were P1 to P5, and the total yield of the saccharides P2 to P5 was as high as 85 w/w % or more, d.s.b.

To separate the saccharides P1 to P5, 3 jacketed stainless steel columns, having an inner diameter of 2.0 cm and a length of one m, were packed with "XT-1016, Na<sup>++</sup>, a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series. The reaction mixture containing any one of saccharides P1 to P5 was separatory applied to the columns at an inner column temperature of 55°C, followed by applying to the columns with 55°C distilled water at a flow rate of SV (space velocity) 0.13. After examining the saccharide composition of the resultant eluate, a fraction containing 97 w/w or more, d.s.b., of any one of saccharides P1 to P5 was recovered and pulverized in vacuo. No substantial reducing power was detected in the purified saccharides P1 to P5 on the Somogyi-Nelson's method.

To identify the saccharides P1 to P5, 50 mg one of which was weighed, dissolved in one ml of 50 mM acetate buffer (pH 4.5), and mixed with one unit of glucoamylase, followed by incubating the mixture at 40°C for 6 hours. High-performance liquid chromatography analysis on the resultant reaction mixture detected glucose and trehalose as shown in Tables 3 and 4. When the saccharides P1 to P5 were subjected to the action of  $\beta$ -amylase, the saccharides P1 and P2 were not hydrolyzed by  $\beta$ -amylase, but the saccharides P3, P4 and P5 were respectively hydrolyzed into one mole of maltose, P2 and one mole of maltose, and P1 and 2 moles of maltose.

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Table 3

Subst	rate	Glucose (%)	Trehalose	Molar ratio*
P	L	36.2	63.8	1.07
P	2	52.0	48.0	2.06
PS	3	61.4	38.6	3.02
P4		68.3	31.7	4.09
P5	5	72.9	27.1	5.11

Note: The molar ratios as indicated with the symbol "\*" are values calculated as moles of glucose against one mole of trehalose.

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Table 4

	Substrate	Glucose (%)	Trehalose (%)	Molar ratio	
	Pl	36.0	64.0	1.07	
٠.	P2	51.5	48.5	2.02	
	P3	61.6	38.4	3.05	
	P4	68.1	31.9	4.06	
	P5	72.5	27.5	5.01	<del></del>

Note: The molar ratios as indicated with the symbol "\*" are values calculated as moles of glucose against one mole of trehalose.

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The results in Tables 3 and 4 strongly show that the saccharides P1 to P5 consist of one mole of trehalose and 1 to 5 moles of glucose. From the facts that glucoamylase specifically hydrolyzes the  $\alpha$ -1,4 and  $\alpha$ -1,6 linkages in maltooligosaccharides and that  $\beta$ -amylase hydrolyzes the a-1,4 linkage in maltooligosaccharides from their end terminals by maltose units, it is estimated that the saccharides P1 to P5 have a structure consisting of glucose or maltooligosaccharide having a degree of glucose polymerization of 2 to 5, both of which have a trehalose residue at their end terminals.

The total judgement of the above results identifies the saccharides P1 to P5 as a-glucosyl trehalose,  $\alpha$ -maltosyl trehalose,  $\alpha$ -maltotriosyl trehalose, a-maltotetraosyl trehalose and  $\alpha$ -maltopentaosyl trehalose respectively, and this evidences that the enzymes have an activity of forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher.

#### Experiment 2-2

# Molecular weight

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In accordance with the method reported by U. K. Laemmli in *Nature*, Vol.227, pp.680-685 (1970), the purified enzymes M-11 and Q36 in Experiment 1 were respectively electrophoresed on sodium dodecyl polyacrylamide gel electrophoresis to give a single protein band at a position corresponding to about 76,000-87,000 daltons. The marker proteins used in this experiment were myosin (MW=200,000 daltons), β-galactosidase (MW=116,250 daltons), phosphorylase B (MW=97,400 daltons), serum albumin (MW=66,200 daltons) and ovalbumin (MW=45,000 daltons).

#### Experiment 2-3

#### Isoelectric point

The purified enzymes M-11 and Q36 obtained in Experiment 1 gave an isoelectric point of about 3.6-4.6 on isoelectrophoresis respectively.

#### Experiment 2-4

#### Optimum temperature

The optimum temperature of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 35-40°C as shown in FIG. 1 or 2 when incubated in usual manner in 50 mM phosphate buffer (pH 7.0) for 60 min.

# Experiment 2-5

# Optimum pH

The optimum pH of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 6.4-7.2 as shown in FIG. 3 or 4 when experimented in usual manner by incubating them at 40°C for 60 min in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

#### Experiment 2-6

#### Thermal stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a temperature of about 35-40°C as shown in FIGs. 5 and 6 when experimented in usual manner by incubating them in 50 mM phosphate buffer (pH 7.0) for 60 min.

#### Experiment 2-7

#### pH Stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a pH of about 5.5-11.0 as shown in FIGs. 7 and 8 when experimented in usual manner by incubating them at 25°C for 16 hours in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

#### Experiment 2-8

#### Amino acid sequence containing the N-terminal

The amino acid sequence containing the N-terminal of the purified enzyme M-11 obtained in Experiment 1 was analyzed on "MODEL 470 A", a gas-phase protein sequencer commercialized by Applied Biosystems, Inc., Foster City, USA, to reveal that nzyme M-11 has an amino acid sequence as shown in SEQ ID NO:12. The amino acid sequence containing the N-terminal of the purified enzyme Q36 was analyzed similarly

as in enzyme M-11 to reveal that it has an amino acid sequence as shown in SEQ ID NO:13.

#### Experiment 2-9

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#### Partial amino acid sequence

An adequate amount of the purified enzyme M-11 obtained in Experiment 1-1 was weighed, dialyzed against 10 mM Tris-HCl buffer (pH 9.0) at 4°C for 18 hours, and admixed with 10 mM Tris-HCl buffer (pH 9.0) to give a concentration of about one mg/ml of the enzyme. About one ml of the resultant solution was placed in a container, admixed with 10 µg lysyl endopeptidase, and incubated at 30°C for 22 hours to partially hydrolyze the enzyme. The resultant hydrolysate was applied to "CAPCELL-PAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Shiseido Co., Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 16 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate at a flow rate of 0.9 ml/min while increasing the concentration of acetonitrile from 16 to 64 v/v % to separatory collect fractions containing a peptide fragment about 28 min or 40 min after the initiation of feeding (the peptide fragments were respectively named "peptide fragment A" and "peptide fragment B"). Fractions containing the peptide fragment A or B were separatory pooled, dried in vacuo, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Similarly as in Experiment 2-8, the peptide fragments A and B were analyzed and revealed to have an amino acid sequence as shown in SEQ ID NO:14 and an amino acid sequence as shown in SEQ ID NO:15.

Similarly as in enzyme M-11, enzyme Q36 obtained in Experiment 1-2 was partially hydrolyzed, and the resultant was fed to "µBONDAPAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Japan Millipore Ltd., Tokyo, Japan, followed by feeding to the column 0.1 v/v % trifluoroacetate containing aqueous acetonitrile raging from a concentration of 24 v/v % to 44 v/v % at a flow rate of 0.9 ml/ml. Fractions containing a peptide fragment eluted about 22 min or about 40 min after the initiation of feeding (the fractions were respectively called "peptide fragment C" and "peptide fragment D" hereinafter) were respectively collected, pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Analyses of the peptide fragments C and D conducted similarly as above revealed that they have amino acid sequences as shown in SEQ ID NOs:16 and 17, respectively.

No enzyme having these physicochemical properties has been known, and this concluded that it is a novel substance. Referring to *Rhizobium* sp. M-11, it is a microorganism which was isolated from a soil of Okayama-city, Okayama, Japan, deposited on December 24, 1992, in National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology, Tsukuba, Ibaraki, Japan, and accepted under the accession number of FERM BP-4130, and it has been maintained by the institute. *Arthrobacter* sp. Q36 is a microorganism which was isolated from a soil of Soja-city, Okayama, Japan, deposited on June 3, 1993, in the same institute, and accepted under the accession number of FERM BP-4316, and it has been maintained by the institute. Japanese Patent Application No.349,216/93 applied by the same applicant discloses the properties and features of the non-reducing saccharide-forming enzyme as well as the detailed bacteriological properties of these microorganisms.

The present inventors energetically screened a chromosomal DNA of *Rhizobium* sp. M-11 by using an oligonucleotide as a probe which had been chemically synthesized based on the partial amino acid sequence of enzyme M-11 as revealed in Experiment 2-9, and found a DNA fragment which consists of 2,316 base pairs having a base sequence as shown in the following SEQ ID NO:1 which initiates from the 5'-terminus. The decoding of the base sequence revealed that the enzyme consists of 772 amino acids as shown in SEQ ID NO:2.

Similarly as in enzyme M-11, a chromosomal DNA of enzyme Q36 was screened by using an oligonucleotide as a probe which had been chemically synthesized based on a partial amino acid sequence of enzyme Q36, and this yielded a DNA fragment having a base sequence consisting of 2,325 base pairs from the 5'-terminus as shown in SEQ ID NO:3. The base sequence was decoded to reveal that enzyme Q36 consists of 775 amino acids and has a partial amino acid sequence containing the N-terminal as shown in SEQ ID NO:4.

The sequential experimental steps used to reveal the base sequence and amino acid sequence as shown in SEQ ID NOs:1 to 4 are summarized as below:

- (1) The enzyme was isolated from a culture of a donor microorganism and highly purified. The purified enzyme was partially hydrolyzed with protease, and the resultant 2 different types of peptide fragments were isolated and determined their amino acid sequences;
- (2) Separately, a chromosomal DNA was isolated from a donor microorganism's cell, purified and partially digested by a restriction enzyme to obtain a DNA fragment consisting of about 3,000-7,000 base pairs. The DNA fragment was ligated by DNA ligase to a plasmid vector, which had been previously cut with a restriction enzyme, to obtain a recombinant DNA;

- (3) The recombinant DNA was introduced into Escherichia coli to obtain transformants, and from which an objectiv transformant containing a DNA encoding the enzyme was selected by the colony hybridization method using as a probe an oligonucleotide which had been chemically synthesized based on the aforesaid partial amino acid sequence; and
- (4) The recombinant DNA was obtained from the transformant and annealed with a primer, followed by allowing a DNA polymerase to act on the resultant to extend the primer, and determining the base sequence of the resultant complementary chain DNA by the dideoxy chain termination method. The comparison of an amino acid sequence estimable from the determined base sequence with the aforesaid amino acid sequence confirmed that the base sequence encodes the enzyme.

As is explained in the above, the enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, is an enzyme which was found as a result of the present inventors' long-term research. The enzyme has distinct physicochemical properties from those of other conventional enzymes. The present invention is to produce the enzyme by applying recombinant DNA technology. The recombinant DNA, and its preparation and uses are explained in detail with reference to examples.

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The recombinant enzyme as referred to in the invention means the whole enzymes which are preparable by recombinant DNA technology and capable of forming non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Generally, the recombinant enzyme according to the present invention has a revealed amino acid sequence, and, as an example, the amino acid sequence, which initiates from the N-terminal as shown in SEQ ID NO:2 or 4, and homologous ones to it can be mentioned. Variants having amino acid sequences homologous to the one as shown in SEQ ID NO:2 or 4 can be obtained by replacing one or more bases in SEQ ID NO:2 or 4 with other bases without substantially alternating the inherent action of the enzyme. Although even when used the same DNA and it also depends on hosts into which the DNA is introduced, ingredients and components of nutrient culture media for culturing transformants, and their cultivation temperature and pH, there may be produced modified enzymes which have amino acid sequences similar to that of SEQ ID NO:2 or 4 as well as having an enzymatic action of the enzyme encoded by the DNA but defecting one or more amino acids located nearness to the N-terminal of the amino acid sequence as shown in SEQ ID NO:2 or 4 and/or having one or more amino acids newly added after the DNA expression to the N-terminal by the modification of intracellular enzymes of hosts. The recombinant enzyme can be obtained from cultures of transformants containing a specific DNA. Examples of such a transformant used in the invention can be prepared by introducing into hosts a DNA having either the base sequence which initiates from the N-terminal or a homologous base sequence to it or a complementary base sequence to them. Such a base sequence may be prepared by replacing one or more bases thereof without alternating the amino acid sequence encoded thereby by using degeneracy of genetic code. Needless to say, one or more bases in the base sequence, which encodes the enzyme or their variants, can be readily replaced with other bases to allow the DNA to actually express the enzyme production in hosts.

The DNA usable in the present invention includes any one of those derived from natural resources and artificially synthesized ones as long as they have such an aforementioned base sequence. The natural resources for the DNA according to the present invention are, for example, microorganisms of the genera Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium and Terrabacter, i.e. Rhizobium sp. M-11 (FERM BP-4130), Arthrobacter sp. Q36 (FERM BP-4316), Brevibacterium helovolum (ATCC 11822), Flavobacterium aquatile (IFO 3772), Micrococcus luteus (IFO 3064), Micrococcus roseus (ATCC 186), Curtobacterium citreum (IFO 15231), Mycobacterium smegmatis (ATCC 19420) and Terrabacter tumescens (IFO 12960) from which genes containing the present DNA can be obtained. The aforementioned microorganisms can be inoculated in nutrient culture media and cultured for about 1-3 days under aerobic conditions, and the resultant cells were collected from the cultures and subjected to ultrasonication or treated with a cell-wall lysis enzyme such as lysozyme or β-glucanase to extract genes containing the present DNA. In this case, a proteolytic enzyme such as protease can be used along with the cell-wall lysis enzyme, and, in the case of treating the cells with an ultrasonic disintegrator, they may be treated in the presence of a surfactant such as sodium dodecyl sulfate (SDS) or may be treated with freezing and thawing. The objective DNA is obtainable by treating the resultant with phenol extraction, alcohol sedimentation, centrifugation, protease treatment and/or ribonuclease treatment used in general in this field. To artificially synthesize the present DNA, it can be chemically synthesized by using the base sequence as shown in SEQ ID NO:1 or 3, or can be obtained in a plasmid form by inserting a DNA which encodes the amino acid sequence as shown in SEQ ID NO:2 or 4 into an appropriate self-replicable vector to obtain a recombinant DNA, introducing the recombinant DNA into an appropriate host to obtain a transformant, culturing the transformant, separating the proliferated cells from the resultant culture, and collecting plasmids containing the DNA from the cells.

Such a recombinant DNA is generally introduced into hosts in a recombinant DNA form. Generally, the recombinant DNA contains the aforesaid DNA and a self-replicable vector, and it can be prepared with a relative easiness by recombinant DNA technology in general when the material DNA is in hand. Examples of such a vector are plasmid vectors such as pBR322, pUC18, Bluescript II SK(+), pUB110, pTZ4, pC194, pHV14, TRp7, TEp7, pBS7, etc.; and phage vectors such as  $\lambda$ gt  $\lambda$ C,  $\lambda$ gt  $\lambda$ B, p11,  $\phi$ 1,  $\phi$ 105, etc. Among these plasmid- and phage-vectors, pBR322, pUC18, Bluescript II SK(+),  $\lambda$ gt  $\lambda$ C and  $\lambda$ gt  $\lambda$ B are satisfactorily used when the present DNA needs to be expressed in *Escherichia coli*, while pUB110, pTZ4, pC194, p11,  $\phi$ 1 and  $\phi$ 105 are satisfactorily used to express the DNA in microorganisms of the genus *Bacillus*. The plasmid vectors pHV14, TRp7, TEp7 and pBS7 are advantageously used when the recombinant DNA is allowed to grow in 2 or more hosts.

The methods used to insert the present DNA into such a vector in the invention may be conventional ones in general in this field. A gene containing the present DNA and a self-replicable vector are first digested by a restriction enzyme and/or ultrasonic disintegrator, then the resultant DNA fragments and vector fragments are ligated. To digest DNAs and vectors, restriction enzymes which specifically act on nucleotides, particularly, type II restriction enzymes, more particularly Sau 3AI, Eco RI, Hind III, Bam HI, Sal I, Xba I, Sac I, Pst I, etc., facilitate the ligation of the DNA fragments and vector fragments. To ligate the DNA fragments with vector fragments, they are annealed if necessary, then subjected to the action of a DNA ligase in vivo or in vitro. The recombinant DNA thus obtained is replicable without substantial limitation by introducing it into appropriate hosts, and culturing the resultant transformants.

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The recombinant DNA thus obtained can be introduced into appropriate host microorganisms including *Escherichia coli* and those of the genus *Bacillus* as well as actinomyces and yeasts. In the case of using *Escherichia coli* as a host, the DNA can be introduced thereinto by culturing the host in the presence of the recombinant DNA and calcium ion, while in the case of using a microorganism of the genus *Bacillus* as a host the competent cell method and the colony hybridization method can be employed. Desired transformants can be cloned by the colony hybridization method or by culturing a variety of transformants in nutrient culture media containing reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and selecting the objective transformants which form non-reducing amylaceous saccharides having trehalose structure as an end unit from the reducing amylaceous saccharides.

The transformants thus obtained extracellularly produce the objective enzyme when cultured in nutrient culture media. Generally, liquid culture media in general supplemented with carbon sources, nitrogen sources and minerals, and, if necessary, further supplemented with small amounts of amino acids and vitamins can be used in the invention. Examples of the carbon sources are saccharides such as starch, starch hydrolysate, glucose, fructose and sucrose. Examples of the nitrogen sources are organic- and inorganic-substances containing nitrogen such as ammonia, ammonium salts, urea, nitrate, peptone, yeast extract, defatted soy been, corn steep liquor, and beef extract. Cultures containing the objective enzyme can be prepared by inoculating the transformants into nutrient culture media, and incubating them at a temperature of 25-65°C and a pH of 2-8 for about 1-6 days under aerobic conditions by aeration and agitation. Such a culture can be used intact as an enzyme agent, and, usually, it may be disrupted prior to use with ultrasonic disintegrator and/or cell-wall lysis enzymes, followed by separating the enzyme from the intact cells and cell debris by filtration and/or centrifugation and purifying the enzyme. The methods to purify the enzyme include conventional ones in general. From cultures intact cells and cell debris are eliminated and subjected to one or more methods such as concentration, salting out, dialysis, separatory sedimentation, gel filtration chromatography, ionexchange chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectric point electrophoresis.

As is described above, the recombinant enzyme according to the present invention has a specific feature of forming non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. The formed non-reducing saccharides have a satisfactorily mild and high-quality sweetness as well as an adequate viscosity and moisture-retaining ability, and, as a great advantageous feature, they can sweeten food products without fear of causing coloration and deterioration because they do not have a reducing residue within their molecule. By using these features a variety of amylaceous saccharides, which have been put aside because of their reducibilities, can be converted into saccharides having a satisfactory handleability and usefulness but having substantially no or extremely-reduced reducibility.

Now explaining the conversion method in more detail, reducing starch hydrolysates, which are obtainable by partially hydrolyzing amylaceous saccharides such as starch, amylopectin and amylose by acids and/or amylases, can be usually used as the substrate for the present recombinant enzyme. Such a starch hydrolysate can be obtained by conventional methods in general used in the art, and examples thereof include one or mor maltooligosaccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltonexaose and maltoheptaose. As described in "Handbook of Amylases and Re-

lated Enzymes", 1st edition, edited by Th. Amylase Research Society of Japan, published by Pergamon Press plc, Oxford, England (1988), α-amylase, maltotetraose-forming amylase, maltopentaose-forming amylase and maltohexaose-forming amylase are especially useful to prepare the reducing amylaceous saccharides used in the invention, and, the use of any one of these amylases readily yields amylaceous saccharide mixtures rich in reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher in a considerably-high yield. If necessary, the combination use of the amylases and starch debranching enzymes such as pullulanase and isoamylase can increase the yield of the reducing amylaceous saccharides used as the substrate for the present recombinant enzyme.

In the conversion method according to the present invention, the present recombinant enzyme is allowed to coexist in an aqueous solution containing one or more of the aforesaid reducing amylaceous saccharides as a substrate, and allowing the solution to enzymatically react at a prescribed temperature and pH until a desired amount of the objective reducing amylaceous saccharides is formed. Although the enzymatic reaction proceeds even below a concentration of 0.1 w/v % of a substrate, a higher concentration of 2 w/v %, preferably, 5-50 w/v % of a substrate can be satisfactorily used to apply the present conversion method to an industrial-scale production. The temperature and pH used in the enzymatic reaction are set within the ranges of which do not inactivate the recombinant enzyme and allow the recombinant enzyme to effectively act on substrates, i.e. a temperature up to about 55°C, preferably, a temperature in the range of about 40-55°C, and a pH of 5-10, preferably, a pH in the range of about 6-8. The amount and reaction time of the present recombinant enzyme are chosen dependently on the enzymatic reaction condition. The enzymatic reaction relatively-highly reduces the reducing power of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, and, in the case of maltopentaose, the reducing powder is lowered to about 7% against the original level.

The reaction mixtures obtained by the present conversion reaction can be used intact, and, usually, they are purified prior to use: Insoluble substances are eliminated from the reaction mixtures by filtration and centrifugation, and the resultant solutions are decolored with an activated charcoal, desalted and purified on ion exchangers, and concentrated into syrupy products. Dependently on their use, the syrupy products are dried in vacuo and spray-dried into solid products. In order to obtain products which substantially consist of non-reducing saccharides, the aforesaid syrupy products are subjected to one or more methods such as chromatography using an ion exchanger, activated charcoal and silica gel for saccharide separation, separatory sedimentation using alcohol and/or acetone, membrane filtration, fermentation by yeasts, and removal and decomposition of reducing saccharides by alkalis. The methods to treat a large amount of reaction mixture are, for example, fixed bed- or pseudomoving bed-ion exchange column chromatography as disclosed in Japanese Patent Laid-Open Nos.23,799/83 and 72,598/83, and such a method produces non-reducing saccharide-rich products in an industrial scale and in a considerably-high yield.

The reducing saccharides thus obtained have a wide applicability to a variety of products which are apt to be readily damaged by the reducibility of saccharide sweeteners: For example, they can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. Since the non-reducing saccharides approximately qualitatively form trehalose when received an enzymatic action of a trehalose-releasing enzyme as disclosed in Japanese Patent Application No.340,343/93, they can be used as an intermediate for the production of trehalose which could not have been readily prepared.

The following examples explain the present invention in more detail, and the recombinant DNA technologies or techniques employed therein are in themselves conventional ones used in the art, for example, those described by J. Sumbruck et al. in "Molecular Cloning A Laboratory Manual", 2nd edition, published by Cold Spring Harbor Laboratory Press, USA (1989).

#### Example 1

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Preparation of recombinant DNA containing DNA derived from enzyme M-11, and transformant

# Example 1-1

# Preparation of chromosomal DNA

A seed culture of *Rhizobium* sp. M-11 was inoculated into bacto nutrient broth medium (pH 7.0), and cultured at 27°C for 24 hours with a rotary shaker. The cells were separated from the resultant culture by centrifugation, suspended in TES buffer (pH 8.0), admixed with 0.05 w/v % lysozyme, and incubated at 37°C for 30 min. The resultant was freezed at -80°C for one hour, admixed with TSS buffer (pH 9.0), heated to 60°C, and admixed with a mixture solution of TES buffer and phenol, and the resultant solution was chilled with ice, fol-

lowed by centrifugally collecting the precipitated crude chromosomal DNA. To the supernatant was added 2 fold volumes of cold ethanol, and the precipitated crude chromosomal DNA was collected, suspended in SSC buffer (pH 7.1), admixed with 7.5 µg ribonuclease and 125 µg protease, and incubated at 37°C for one hour. Thereafter, a mixtur—solution of chloroform and isoamyl alcohol was added to the reaction mixture to extract the objective chromosomal DNA, and admixed with cold ethanol, followed by collecting the formed sediment containing the chromosomal DNA. The purified chromosomal DNA thus obtained was dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the solution was freezed at -80°C.

#### Example 1-2

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# Preparation of recombinant DNA pBMT7 and transformant BMT7

About one ml of the purified chromosomal DNA obtained in Example 1-1 was placed in a container, admixed with about 35 units of *Sau* 3AI, a restriction enzyme, and enzymatically reacted at 37°C for about 20 min to partially digest the chromosomal DNA, followed by recovering a DNA fragment consisting of about 3,000-7,000 base pairs by sucrose density-gradient ultracentrifugation. One µg of Bluescript II SK(+), a plasmid vector, was provided, subjected to the action of *Bam* HI, a restriction enzyme, to completely digest the plasmid vector, admixed with 10 µg of the DNA fragment and 2 units of T4 DNA ligase, and allowed to stand at 4°C overnight to ligate the DNA fragment to the vector fragment. To the resultant recombinant DNA was added 30 µl of "Epicurian Coli® XLI-Blue", competent cell commercialized by Toyobo Co., Ltd., Tokyo, Japan, allowed to stand under ice-chilled conditions for 30 min, heated to 42°C admixed with SOC broth, incubated at 37°C for one hour to introduce the recombinant DNA into *Escherichia coli*.

The resultant transformant was inoculated into agar plate (pH 7.0) containing 50  $\mu$ g/ml of 5-bromo-4-chloro-3-indolyl- $\beta$ -galactoside, and cultured at 37°C for 18 hours, followed by placing a nylon film on the agar plate to fix thereon about 4,400 colonies formed on the agar plate. Based on the amino acid sequence of Pro-Glu-Trp-Glu-Lys located at positions from 17 to 21 in the amino acid sequence of the peptide fragment A as revealed in Experiment 2-9, the base sequence of probe 1 as shown in SEQ ID NO:5 was chemically synthesized, labelled with <sup>32</sup>P, and hybridized with the colonies of transformants fixed on the nylon film, followed by selecting 9 transformants which exhibited a strong hybridization.

The objective recombinant DNA was selected in usual manner from the 9 transformants, and, in accordance with the method described by E. M. Southern in *Journal of Molecular Biology*, Vol.98, pp.503-517 (1975), hybridized with probe 2 having the base sequence as shown in SEQ ID NO:6 which had been chemically synthesized based on the amino acid sequence of Thr-Glu-Phe-Trp-Asp located at positions from 16 to 20 in the amino acid sequence of the peptide fragment B as revealed in Experiment 2-9, followed by selecting a recombinant DNA which strongly hybridized with probe 2. The recombinant DNA and transformant thus selected were respectively named pBMT7 and BMT7.

The transformant BMT7 obtained in the above was inoculated into L-broth (pH 7.0) containing 100 µg/ml ampicillin, and cultured at 37°C for 24 hours with a rotary shaker. After completion of the culture, the cells were collected from the culture by centrifugation, and treated with the alkaline method in general to extracellularly extract a recombinant DNA. The resultant was in usual manner purified and analyzed to find that the recombinant DNA pBMT7 consists of about 9,300 base pairs and has a structure expressed by the restriction map as shown in FIG. 9. It was revealed that as shown in FIG. 9 the DNA consisting of 2,316 base pairs encoding enzyme M-11 is located in the downstream near to the digested site by *Pst* I, a restriction enzyme.

#### Example 1-3

#### Production of enzyme by transformant

A liquid medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50  $\mu$ g/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture of transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 37°C for 24 hours with a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 3,000 units of the enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue or *Rhizobium* sp. M-11 was inoculated into a fresh preparation of the same liquid culture medium but free of ampicillin, and, in the case of the culture of *Rhizobium* sp. M-11, it was cultured and treated similarly as above except that the culturing temperatur was set to 30°C.

Assaying the resultant activity, one L culture of *Rhizobium* sp. M-11 yielded about 1,500 units of the enzyme, and the yield was significantly lower than that of transformant BMT7. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as that of Experiment 2 showing a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on isoelectrophoresis. The results indicate that the present enzyme can be prepared by recombinant DNA technology, and the yield is significantly increased thereby.

#### Example 2

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# Preparation of complementary DNA derived from enzyme M-11 and determination of its base sequence and amino acid sequence

Two  $\mu g$  of the recombinant DNA pBMT7 obtained by the method in Example 1-2 was weighed, admixed with 2 M aqueous sodium hydroxide solution to effect degeneration, and admixed with an adequate amount of cold ethanol, followed by collecting the resultant sediment containing a template DNA and drying the sediment in vacuo. To the template DNA were added 50 pmole/ml of a chemically synthesized primer 1 having the base sequence as shown in SEQ ID NO:7, and 10  $\mu$ l of 40 mM Tris-HCl buffer (pH 7.5) containing 20 mM magnesium chloride and 50 mM sodium chloride, and incubated at 65°C for 2 min to effect annealing, and the mixture was admixed with 2  $\mu$ l of an aqueous solution containing dATP, dGTP and dTTP in respective amounts of 7.5  $\mu$ M, 0.5  $\mu$ l of [ $\alpha$ -32P]dCTP (2 mCi/ml), one  $\mu$ l of 0.1 M dithiothreitol, and 2  $\mu$ l of 1.5 units/ml T7 DNA polymerase, followed by incubating the resultant mixture at 25°C for 5 min to extend the primer 1 from the 5'-terminus to the 3'-terminus. Thus, a complementary chain DNA was formed.

The reaction product containing the complementary chain DNA was divided into quarters, to each of which 2.5  $\mu$ l of 50 mM aqueous sodium chloride solution containing 80  $\mu$ M dNTP and 8  $\mu$ M ddATP, ddCTP, ddGTP or ddTTP was added, and the resultant mixture was incubated at 37°C for 5 min, followed by suspending the reaction by the addition of 4  $\mu$ l of 95 v/v % aqueous formamide solution containing 20 mM EDTA, 0.05 w/v % bromophenol blue and 0.05 w/v % xylene cyanol. The reaction mixture was placed in a container, heated in a boiling-water bath for 3 min, placed on a gel containing 6 w/v % polyacrylamide, and electrophoresed by energizing the gel with a constant voltage of about 2,000 volts to separate DNA fragments, followed by fixing the gel in usual manner, drying and subjecting the resultant gel to autoradiography.

Analyses of the DNA fragments separated on the radiogram revealed that the complementary chain DNA contains the base sequence consisting of 2,936 base pairs as shown in SEQ ID NO:10. An amino acid sequence estimable from the base sequence was as shown in SEQ ID NO:10, and it was compared with the amino acid sequence containing the N-terminal and the partial amino acid sequence of enzyme M-11 as shown in SEQ ID NO:12, 14 or 15, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:12 corresponded to the amino acid sequence at positions from 1 to 20 of SEQ ID NO:10, and the partial amino acid sequence of SEQ ID NO:14 or 15 corresponded to the amino acid sequence at positions from 486 to 506 or at positions from 606 to 626 of SEQ ID NO:10. The results indicate that the enzyme produced from *Rhizobium* sp. M-11 has the amino acid sequence of SEQ ID NO:2, and the enzyme derived from the microorganism is encoded by the DNA having the base sequence as shown in SEQ ID NO:1.

#### Example 3

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Preparation of recombinant DNA containing DNA derived from Arthrobacter sp. Q36 and transformant

#### Example 3-1

#### Preparation of chromosomal DNA

Similarly as in Example 1-1, a chromosomal DNA was isolated from *Arthrobacter* sp. Q36, purified and dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the resultant solution was freezed at -80°C.

#### Example 3-2

# Preparation of recombinant DNA pBQT13 and transformant BQT13

The purified chromosomal DNA obtained in Example 3-1 was partially digested similarly as in Example 1-2, followed by recovering a DNA fragment consisting of about 3,000-6,000 base pairs by sucrose density gradient ultracentrifugation. The DNA fragment was ligated to a lysate of Bluescript II SK(+) which had been treated with *Bam* HI similarly as in Example 1-2, and the resultant recombinant DNA was introduced into *Escherichia coli* XLI-Blue. The transformants thus obtained were cultured similarly as in Example 1-2 in an agar plate containing 5-bromo-4-chloro-3-indolyl-β-D-galactoside, and the resultant about 4,500 colonies were fixed on a nylon film, while probe 3 having the base sequence as shown in SEQ ID NO:8 was chemically synthesized based on the amino acid sequence as expressed by Phe-Asp-Val-Asp-Trp-Asp, which are located at positions from 11 to 16 in the amino acid sequence of the peptide fragment D as shown in SEQ ID NO:17, labelled with <sup>32</sup>P, and hybridized with transformant colonies which had been fixed on the nylon film, followed by selecting 8 transformants which strongly hybridized with probe 3.

Similarly as in Example 1-2, the objective recombinant DNA was selected from the 8 transformants, and hybridized with probe 4 having the base sequence as shown in SEQ ID NO:9 which had been chemically synthesized based on the amino acid sequence located at positions from 16 to 20, i.e. Thr-Glu-Phe-Trp-Asp, in SEQ ID NO:16, followed by selecting a recombinant DNA which strongly hybridized with probe 4. The recombinant DNA and transformant thus selected were respectively named pBQT13 and BQT13.

The transformant BQT13 was inoculated into L-broth containing amplicillin, and cultured similarly as in Example 3-2, and the proliferated cells were collected from the resultant culture, and from which a recombinant DNA was extracted, purified and analyzed to reveal that the recombinant pBQT13 consists of about 7,200 base pairs and has a structure expressed by the restriction map as shown in FIG. 10. As shown in FIG. 3, it was reveal that the DNA, which consists of 2,325 base pairs and encodes the DNA of enzyme Q36, is located in the downstream near the cleavage site of *Xmn* I.

#### Example 3-3

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#### Production of enzyme by transformant BQT13

A liquid culture medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 µg/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture of the transformant BQT13 obtained in Example 3-2, followed by culturing the transformant at 37°C for 24 hours by a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 2,450 units of the enzyme.

As a control, Escherichia coli XLI-Blue or Arthrobacter sp. Q36 was inoculated in a fresh preparation of the same liquid culture medium but free of ampicillin, and cultured and treated similarly as above except that the culturing temperature was set to 30°C. The assay of the activity of the resultants showed that one L of the culture of Arthrobacter sp. Q36 yielded about 1,200 units of the enzyme, and the level of which was significantly lower than that of the transformant BQT13. Escherichia coli XLI-Blue used as a host dld not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 was purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as shown in Experiment 2 of a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on isoelectrophoresis.

The results indicate that the enzyme can be prepared by recombinant DNA technology, and the yield might be significantly increased thereby.

#### Example 4

Preparation of complementary chain DNA derived from Arthrobacter sp. Q36, and determination of its base sequence and amino acid sequence

The recombinant DNA pBQT13 obtained in Example 3-2 was similarly treated as in Example 2 to form a template DNA which was then anneal d together with the primer 1, followed by allowing T7 DNA polymerase

to act on the resultant to ext nd the primer 1 from the 5'-terminus to 3'-terminus to obtain a complementary chain DNA. Similarly as in Example 2, the complementary chain DNA was subjected to the dideoxy chain terminator method to analyze DNA fragments isolated on a radiogram. The result revealed that the complementary chain DNA contained a base sequence consisting of 3,073 base pairs and an amino acid sequence estimable from the base sequence were as shown in SEQ ID NO:11. The amino acid sequence was compared with respect to the amino acid sequence containing the N-terminal and the partial amino acid sequence of SEQ ID NO:13, 16 or 17, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:13 corresponded to that located at positions from 1 to 20 in SEQ ID NO:11, and the partial amino acid sequence of SEQ ID NO:16 and 17 corresponded to the amino acid sequence located at positions from 606 to 625 or from 110 to 129 in SEQ ID NO:11. The results indicate that enzyme Q36 has the amino acid sequence of SEQ ID NO:4, and it is encoded by the DNA having the base sequence as shown in SEQ ID NO:3.

#### Example 5

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# Preparation of recombinant enzyme

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate, and to each flask was added 50 µg/ml ampicillin and autoclaved at 120°C for 20 min. Thereafter, the flasks were cooled and inoculated with the transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 27°C for 24 hours by a rotary shaker. Apart from this, 18 L of a fresh preparation of the same liquid culture medium was placed in an Erlenmeyer flask, admixed with 50 µg/ml ampicillin, sterilized at 120°C for 20 min, cooled and inoculated with one v/v % of the seed culture obtained in the above, followed by the culture at 37°C for 24 hours under aeration and agitation conditions. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to show that one L of the culture yielded about 3,000 units of the enzyme. The supernatant was purified by the method in Experiment 1-1 to obtain an about 50 ml aqueous solution containing about 135 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

# Example 6

# Preparation of recombinant enzyme

Recombinant BQT13 obtained by the method in Example 3-2 was cultured similarly as in Example 5, and the resultant culture was treated with an ultrasonic integrator to disrupt cells. The resultant suspension was centrifuged to remove insoluble substances, and the resultant supernatant was assayed for the enzyme activity to reveal an enzyme production of about 2,450 units per L of the culture. The supernatant was purified by the method in Experiment 1-1 to obtain an about 45 ml aqueous solution containing about 120 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

#### Example 7

# Conversion of starch hydrolysate by recombinant enzyme

A potato starch was suspended in water to give a 6 w/w % suspension which was then autoclaved at 120°C for 10 min to gelatinize the starch. The gelatinized starch was rapidly cooled to 50°C, adjusted to a pH of about 4.5, admixed with 2,500 units/g starch, d.s.b., of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 50°C for 20 hours. The reaction mixture was adjusted to pH 6.0, autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with 150 units/g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 45°C for 24 hours to obtain a reaction mixture containing r ducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The reaction mixture was autoclaved at 120°C for 20 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with one unit/g starch, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 96 hours. The resultant reaction mixture was heated at 96°C for 10 min to inactivate the remaining enzyme, cooled and filt red, and the resultant filtrate was in usual manner decolored with an activated charcoal, de-

salted and purified by an ion exchanger and concentrated to obtain an about 70 w/w % syrup, d.s.b., in a yield of about 91%, d.s.b.

Analysis of the syrup conducted by the method of Experiment 2-1 revealed that it had a DE (dextrose equivalent) of 18.7 and contained as a main component, on a dry solid basis, 8.4 w/w % α-glucosyl trehalose, 5.6 w/w % α-maltosyl trehalose, 37.9 w/w % α-maltotriosyl trehalose, and that the greater part of the aforesaid reducing saccharides were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

#### Example 8

# Conversion of starch hydrolysate by recombinant enzyme

Potato starch was suspended in water to give a concentration of 33 w/w %, d.s.b., and the suspension was admixed with 0.1 w/w % calcium carbonate, d.s.b. The resultant suspension was admixed with 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled, admixed with 5 units/g starch, d.s.b., of a maltotetraose-forming amylase derived from Pseudomonas stutzen as disclosed in Japanese Patent Laid-Open No.240,784/88, and enzymatically reacted at 55°C for 6 hours. Thereafter, the resultant reaction mixture was admixed with 30 units/g starch, d.s.b., of "α-amylase 2A", an α-amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and enzymatically reacted at 65°C for 4 hours to form about 50 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The resultant mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.5 and contained as a main component 3.8 w/w %  $\alpha$ -glucosyl trehalose, 43.8 w/w % a-maltosyl trehalose, and 1.2 w/w %  $\alpha$ -maltotriosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

# Example 9

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# Conversion of maltopentaose by recombinant enzyme

A high-purity maltopentaose produced by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, was dissolved in water to give a concentration of 20 w/w %, d.s.b., and the solution was adjusted to pH 6.5, admixed with one unit/g maltopentaose, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at 45°C for 48 hours. The reaction mixture was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, concentrated and analyzed by the method in Experiment 2-1 to find that about 92 w/w %, d.s.b., of the material maltopentaose was converted into α-maltotriosyl trehalose.

Four jacketed-stainless steel columns, having a diameter of 5.4 cm and a length of 5 m each, were packed to homogeneity with "XT-1016 (Na<sup>+</sup>-form)", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series to give a total column length of 20 m. The reaction mixture obtained in the abov was fed to the columns at a rate of about 5 v/v % against the resin at an inner column temperatur of 55°C, and the columns were fed with 55°C hot water at an SV (space velocity) of 0.13 to elute saccharide components. Based on the saccharide composition analysis of the eluate,

fractions rich in non-reducing saccharides were collected, pooled, concentrated, dried in vacuo and pulverized to obtain a solid product in a yield of about 55%, d.s.b.

Analysis of the solid product by the method in Experiment 2-1 revealed that it had a DE less than about 0.2 and contained 99.0 w/w %  $\alpha$ -maltotriosyl trehalose, d.s.b. The product, having a relatively-low hygroscopicity, a significantly-low reducibility as well as a slight sweetness, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

#### Example 10

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#### Conversion of starch hydrolysate by recombinant enzyme

"PINE-DEX #4", a starch hydrolysate produced by Matsutani Chemical Ind., Co., Ltd., Kyoto, Japan, was dissolved in water to give a concentration of 40 w/w %, d.s.b., and the solution was heated to 45°C, adjusted to pH 6.5, admixed with one unit/g starch hydrolysate, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at for 96 hours to obtain a reaction mixture containing non-reducing saccharides having trehalose structure as an end unit. Thereafter, the reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, concentrated up to a 20 w/w % solution, d.s.b., cooled to 55°C, adjusted to pH 4.5, admixed with 10 units/g saccharide, d.s.b., of "GLUCOZYME", a glucoamylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, and enzymatically reacted for 40 hours. The reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, cooled, decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain an about 60 w/w % syrupy product containing about 29.7 w/w % trehalose, d.s.b.

Similarly as in Example 9 except for using "CG6000 (Na<sup>+</sup>-form), the syrupy product was fractionated, followed by collecting fractions containing about 90 w/w % trehalose, d.s.b. The fractions were pooled, concentrated into an about 75 w/w % solution which was then transferred to a crystallizer, admixed with about 2 w/w % trehalose hydrate as a seed crystal against saccharides, d.s.b., and crystallized under gentle stirring conditions to obtain a masseculte with a crystallinity of about 45%. The masseculte was sprayed downward from a nozzle, equipped at the upper part of a spraying tower at a pressure of about 150 kg/cm² while about 85°C hot air was flowing downward from the upper part of the tower to accumulate a crystalline powder on a belt conveyer provided on the basement of the tower, followed by gradually transferring it out of the tower. Thereafter, the powder was transferred to an aging tower and aged for 10 hours to complete the crystallization and drying while an about 40°C hot air was blowing to the contents.

The product, having a substantial non-hygroscopicity and a mild and high-quality sweetness, can be satisfactorily used in food products, cosmetics, pharmaceuticals and feeds as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

# Example 11

# Conversion of starch hydrolysate by recombinant enzyme

Tapioca starch was suspended in water to give a concentration of 34 w/w % and admixed with 0.1 w/w % calcium carbonate. To the suspension was added 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an αamylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min to liquefy the starch. The liquefied product was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 55°C, adjusted to pH 5.2, admixed with 10 units/g starch, d.s.b., of "α-amylase 2A", an α-amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and 500 units of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 55°C for 20 hours to form a mixture with a DE of about 29, containing about 60 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose and maltohexaose. The mixture was autoclaved at 120°C for 10 min to inactivate the remaining nzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 15.8 and contained as a main component 5.8 w/w %  $\alpha$ -glucosyl trehalos , 8.5 w/w % a-maltosyl trehalose, 13.1 w/w %  $\alpha$ -maltotriosyl trehalose, 18.9 w/w %  $\alpha$ -maltotetraosyl trehalose and 3.6 w/w %  $\alpha$ -maltopentaosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 12

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# Conversion of starch hydrolysate by recombinant enzyme

Similarly as in Example 8, a liquefied potato starch was successively subjected to the action of maltote-traose-forming amylase and  $\alpha$ -amylase to form a mixture containing about 50 w/w %, d.s.b, of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltote-traose and maltopentaose. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled and filtered, and the filtrate was decolored in usual manner with an activated charcoal, desalted and purified with an ion exchanger, and concentrated to obtain an about 70 w/w % syrupy product in a yield of about 90 w/w % against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.3 and contained as a main component 3.6 w/w %  $\alpha$ -glucosyl trehalose, 44.0 w/w %  $\alpha$ -maltosyl trehalose and 1.0 w/w %  $\alpha$ -maltotriosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained in the syrupy product were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

As is described above, the present invention is based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher. The present invention is to explore a way to produce such enzyme by recombinant DNA technology in a relatively-large scale and in a considerably-high yield. The conversion method using the present recombinant enzyme effectively converts reducing amylaceous saccharides into their corresponding non-reducing saccharides which have a mild and high-quality sweetness and an adequate viscosity and moisture-retaining ability, do not have a reducing residue within the molecules, and sweeten food products without fear of causing an unsatisfactory coloration and deterioration. In addition, the present recombinant enzyme is the one with a revealed total amino acid sequence, and because of this it can be used for the preparation of trehalose and non-reducing saccharides having trehalose structure as an end unit which are premised on being used in food products without fear of causing side effects.

Thus, the present invention is a significant invention which exerts the aforesaid outstanding action and effect as well as giving a great contribution to the field.

While there has been described what is at present considered to be the preferred embodiments of the invention, it will be understood the various modifications may be made therein, and it is intended to cover in the appended claims all such modifications as fall within the true spirits and scope of the invention.

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#### SEQUENCE LISTING

# (1) GENERAL INFORMATION: المراشين والمراسطين المشارك والأراث

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Dumpada karboro ackapad gross sea Wilson 生物 医电子关键 医电路

# (i) APPLICANT:

NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO

....

(ii) TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES

#### (iii) NUMBER OF SEQUENCES:17

ranamin de dinazione in la company

# (iv) ADDRESS:

- (A) ADDRESSEE: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
- (B) STREET:2-3, 1-CHOME, SHIMOISHII
  (C) CITY:OKAYAMA
  (E) COUNTRY:JAPAN
- (F) POSTAL CODE (ZIP):700

#### (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE:Floppy disk
- (B) COMPUTER: IBM PC compatible
  (C) OPERATING CYCENTERS
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS

# (vii) PRIOR APPLICATION DATA:

- (A1) APPLICATION NUMBER: JP 47940/1994
- (B1) FILING DATE: February 23, 1994
  (A2) APPLICATION NUMBER: JP 47956/1994
- (B2) FILING DATE: February 23, 1994
  - (A3) APPLICATION NUMBER: JP 90705/1994
  - (B3) FILING DATE:April 6, 1994
    (A4) APPLICATION NUMBER:JP 90728/1994
  - (B4) FILING DATE: April 6, 1994

# (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2316 base pairs
  - (B) TYPE: nucleic acid
  - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATCCTGAAGG	CAGAGAGCGG	CTCCGACCAC	GGCTATGACG	TCACCGATCC	CGCCGTAGTG	180
GACCCGGAGC	GCGGCGGCCC	TGAAGGGCTG	GCCGCGGTGT	CCAAGGCGGC	CCGCGGTGCC	240
GGCATGGGCG	TGCTGATCGA	CATCGTGCCG	AACCACGTGG	GCGTGGCGTC	GCCGCCGCAG	300
AACCCGTGGT	GGTGGTCGCT	GCTCAAGGAA	GGGCGCGGGT	CGCCCTACGC	CGTGGCGTTC	360
GACGTCGACT	GGGACCTGGC	GGGGGCCGC	ATCCGGATCC	CCGTCCTGGG	CAGCGACGAC	420
GATCTGGACC	AGCTCGAAAT	CAAGGACGGC	GAGCTGCGGT	ACTACGACCA	CCGCTTCCCG	480
CTGGCCGAGG	GCAGCTACCG	GGACGGCGAC	TCCCCGCAGG	ACGTCCACGG	CCGGCAGCAC	540
TACGAACTCA	TCGGCTGGCG	GCGCGCCGAC	AATGAACTGA	ACTACCGCCG	GTTCTTCGCG	600
GTGAACACGC	TCGCCGGCAT	CCGGGTGGAG	GTGCCGCCGG	TCTTCGATGA	AGCGCACCAG	660
GAGGTGGTGC	GCTGGTTCCG	TGCGGGGCTC	GCCGACGGGC	TGCGGATCGA	CCACCCGGAC	720
GGCCTGGCCG	ATCCCGAGGG	GTATTTGAAG	CGGCTCCGTG	AGGTCACCGG	GGGCGCGTAC	780
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GACATGATCC	GCGGGACCAA	GCGCCGGATC	ACCGACGGCA			1020
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# (3) INFORMATION FOR SEQ ID NO:2:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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                                               335
    Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
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    Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
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                              450
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     515 520 525
Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
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                                                 540
          530
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                       550
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     Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
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                         585
     His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
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                   600
     Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
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     Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
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                       635
     Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
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                                    655
                650
     Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
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        665
                            670
     Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
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                    685
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<sup>(4)</sup> INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2325 base pairs
     (B) TYPE: nucleic acid
     (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC
GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTT CCAAGGCGGC CCGCGCGCGGG
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGCGCGAG
                                                                                                                                                                                                         120
                                                                                                                                                                                                         180
10
            GGCATGGGCG TGCTGATCGA CATCGTGCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540
TACGAGCTCA TCGGCTGGCG CCGCGGGAC AACGACCTG ACTACCGCCG CTTTTTCGCG 660
GTGAACACGC TCGCCGGGT CCGCGGGAC ATCCCCGCG TCTTCGACGA GGCACACCAG 660
GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGCC TGCGGATCGA CCACCCGGAC 720
GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACCCGGG AAGTCACCGG CGGCGCTTAC 780
GTGCTGATCG AAAGATCCT GGAGCCGGC GAGCACCTGC CCGCCAGCTT CGAGTGTAA 840
           20
25
35
              GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
              TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA
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(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775

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(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr 10 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp 30 25 20 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly 35 40 45 50
Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu 55 60 65
Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu 60 65 75 70

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     Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
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                                 110
     Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
                                             130
                         125
     Gly Ser Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
                                    145
                                                        150
               140
     Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
    155 160 165 170
Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
                                              165
                                     180
                                                            185
                   . 175 .
     Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
                                 195
                                                    200
     Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
            .190
                                            215
                         210
     Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
                                                        235
                                     230
                 225
     Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
                                                250
                             245
     Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
20
                                                            270
                                         265
                     260
     Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
                                                     285
                                280
     275
     Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
                                            300
                         295
     Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
25
                                                         320 กร้างคริกักย์เกา
          310
                                     315
     Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
                                               335
                             330 -
     Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
                                                             355
                                       ...:350
                    345
      Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
                                                     370
                                 365.
             360 .
      Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
                                             385
                         380
      Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu
                                                        405
                                400
               395
      Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
                                                420
                            415
      Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
                                         435
                     430 -
      Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
                                                     455
                                 450
             445
      Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
40
                                              470
                          465
      Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
                                                         490
                                      485
                  480
      Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
                                                 505
                              500
      Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
45
                                         520
                     515
      Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
                                                    540
                                  535
      Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
                        550
                                             555
      Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
                                                         575
                                      570
                  565
      Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
                                                 590
                             585
      Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
                                          605
                      600
      Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
55
                                  620
```

	Asp 630	Pro	Asp	Asn	Arg	Arg 635	Pro	Phe	Ser	Phe	Asp 640	Asp	Arg	Arg	Ala	Ala 645	Leu
5	Glu	Gln	Leu	Asp 650	Ala	Gly	Asp	Leu	Pro 655	Ala	Ser	Phe	Thr	Asp 660	Glu	Arg	Thr
		Leu 665	Leu	Val	Thr	Ser	Arg 670	Ala	Leu	Arg	Leu	Arg 675	Arg	Asp	Arg	Pro	Glu 680
					685			•	Leu	690					695	-	
10			700					705	Ala				710				
	715					720	_		Glu		725					730	
				735					Lys 740					745	-	_	
15	_	750	_			_	755		Asp		Phe	Arg 760	Ser	Phe	Pro	Val	<b>Ala</b> 765
	Leu	Leu	Val	Pro	770	Thr	Gly	Gly	Glu	Ser 775						. · · - . Υ. ·	·- ·-
20	(6)	TNE	יבאמר	er ( ) i	EOD	CEO	<b>TD</b> 1	10 . F	_								
			JRMA.	LION	FOR	SEQ	ו עד	KO: 5	:			_					
25	(i)	(A)	LEI TYI	NGTH : PE : nu RANDE	:14 h iclei EDNES	TERI pase lc ac SS:si nknov	pair cid ingle	rs							•		
	(ii)		ECUI		PE : 0	other	r ἡu	clei	c aci	id							
30	(xi)	SEC	QUENC	CE DE	ESCRI	CPTIC	ON: S	SEQ :	ID NO	):5:							
	CCN	GARTO	GG 1	ARAA										_	-		14
	-	_ :					· - ·	-									
35	(7)	INFO	ORMAT	rion	FOR	SEQ	ID 1	NO : 6	•					·			
40	(i)	(A) (B) (C)	LEI TYI STI	NGTH : PE : nu RANDE	:14 h iclei EDNES	TERI base ic ac SS:si iknov	pair cid ingle	rs									
	(ii)	MOI (A)	LECUI pro	LE TY	PE:c	other	nuo	cleid	c aci	id					-		
45	(xi)	SEC	QUENC	CE DE	ESCRI	PTIC	ON: S	SEQ :	ED NO	0:6:							
	ACNO	SARTI	TYT (	GGA	,												14
	(8)	INFO	ORMA	NOIT	FOR	SEQ	ID 1	10:7	:		-						
50	(i)	(A) (B) (C)	LEN TYP	NGTH : PE : nu RANDE	17 k iclei DNES	TERI Dase Ic ac SS:si	pair id ingle	rs									

.3

(ii) MOLECULE TYPE:other nucleic acid
(A) primer

55

		•	-	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:			
5	GTAAAACGAC GGCCAGT		::17	
	O'AMARCOAC OOCCATO.		.31	•
			. **	
	(9) INFORMATION FOR SEQ ID NO:8:			
	(i) SEQUENCE CHARACTERISTICS:			
10	(A) LENGTH:17 base pairs	• •	•	
	(B) TYPE:nucleic acid			
	(C) STRANDEDNESS:single		•	•
	(D) TOPOLOGY: unknown			
	(ii) MOLECULE TYPE:other nucleic acid			
15	(A) probe	•		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:			
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO.8.			
	TTYGAYGTNG AYTGGGA	•	<b>~"17</b>	
			-	
20	(10) INFORMATION FOR SEQ ID NO:9:			
	(10) Intoldanton for DDR 12 more		•	•
	(i) SEQUENCE CHARACTERISTICS:	•	•	
	(A) LENGTH:14 base pairs (B) TYPE:nucleic acid			
25	(C) STRANDEDNESS:single			
23	(D) TOPOLOGY: unknown			
	(1) ) was marked market above and laid and			
	<pre>(ii) MOLECULE TYPE:other nucleic acid   (A) probe</pre>			
	(R) Plobe			
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:			•
	ACNGARTTYT GGGA		.14	
**	ACHORITIE COOL		•	
	// TIMORIA MICH. BOD. CHO. ID. NO. 10			
• •	(11) INFORMATION FOR SEQ-ID NO:10: (i) SEQUENCE CHARACTERISTICS:			
35	(A) LENGTH: 2936 base pairs			
	(B) TYPE: nucleic acid	Sp. 15	4 4	
	(C) strandedness:double			
	(D)TOPOLOGY:linear (ii)MOLECULE TYPE:genomic DNA			
	(vi) ORIGINAL SOURCE:		~	
40	(A) ORGANISM: Rhizobium sp.			
•.	(B) INDIVIDUAL ISOLATE:M-11 (FERM	BP-4130)		
	(ix) FEATURE: (A) NAME/KEY:5'UTR			
	(B) LOCATION: 1564			
	(C) IDENTIFICATION METHOD: E		•	
45	(A) NAME/KEY: mat peptide			
	(B)LOCATION:5652880 (C)IDENTIFICATION METHOD:S			
	(A) NAME/KEY: 3'UTR			
-	(B) LOCATION: 28812936			
F.O.	(C) IDENTIFICATION METHOD: E			
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:		~ * *	
	CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC	AAGCTCCCGT	CGGATGAATA	60
	CGCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG	GGTGCCGATT	CCGAACCCGT	120
	GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC	GTGGTGCTCC	TGACGCACAG	180 240
	CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC	CICGCAGCCGA	GGAAGACCAA	300

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GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA
GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC
     GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA
     AGGCAAGCAG GGCGGGACGG GCTC
                                                                         564
     ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC
     Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
                                         . 10
10
     ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG
                                                                          660
     Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
                                     25
     GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC
     Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
                                  40
     GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC
                                                                          756
     Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
                                                  . 60
                              55
     GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC
     Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
20
     65.
     GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG
     Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
                     85
                                          90
     TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTC AAG GAA GGG CGC C9000
     Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
     25
     Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
             115
                                  120
                                                       125
     GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG Gly Arg Tle Arg Tle Pro Val Leu Gly Ser Asp Asp Leu Asp Gln
                              135
     CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG
                                                                         1044
     Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro-
                          150
                                              155
     CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC
     Leu Ala Glu Gly Ser Tyr-Arg Asp Gly Asp Ser Pro Gln Asp Val His
                     165
                                         170
     GGC CGG CAC TAC GAA CTC ATC GGC TGG CGC GCC GAC AAT GAA
     Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
                                                           190
                                      185
     CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG
                                                                         1188
     Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg
             195
                                  200
                                                       205
40
     GTG GAG GTG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC
                                                                         1236
     Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg
                              215
                                                   220
     TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC
                                                                         1284
     Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
     225
                          230
                                              235
                                                                   240
     GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                                                                         1332
                      245
                                          250
     GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG
                                                                         1380
     Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
                 260
                                      265
                                                           270
     TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC
                                                                         1428
     Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
             275
                                  280
                                                       285
     GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG
                                                                         1476
     Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
         290
                              295
                                                   300
     GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG
                                                                         1524
55
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Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
                                                                       320
                                                 315
                           310 -
     305
     GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC GG 1572
     Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                                                                   335
                                             330
                       325
     TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT | 1620
     Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
                                        345
     CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC
     Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
                                                          365
                                    360
              355
     CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG
                                                                              1716
     Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
                                375
          370
     GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC
15
     Ala Cys Asp Leu Ala Ala Arg Arg Pro Glu Leu Gly Gln Thr Val
                                                 395
                           390
     CAG CTG CTG CAG. CCG CTG CTG CTG GAT. ACC GAC. CTC GAG ATT. TCC .CGC
                                                                              1812
     Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
                       405.
                                             410
     AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
                                                                              1860
                                         425
                   420
     ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC
     Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
                                                          445
                                    440
     GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
                                455
                                                      460
     ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
                                                                              2004
                                                                        480.
                                                  475
                            470
     ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
                                             490
                       485
     ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC
      Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
                                                               510
                                         505
     ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG
                                                                               2148
35
      Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
                                     520
                                                          525
              515
      GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC
                                                                               2196
     Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
                                                      540
                                535
      GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT
                                                                               2244
     Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
                                                                        560
                                                  555
                            550
      CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC
      Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
                                              570
                       565
      TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC
      Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
45
                                                               5'90
                                         585
                   580
      CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG
                                                                               2388
      Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
                                                           605
                                     600
               595
      CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG
      Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
                                                       620
                                 615
      GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC
                                                                               2484
      Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
                                                  635
                          630.
      GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC
                                                                               2532
      Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
55
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650

645

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TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG
      Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
      CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
                                                                                            2628
                                                                    685
                                          680
      CAT GCC AGG GGC CCC GCC GGC GGC CAC CTG GTG GCG TTC GAC CGC GGC
      His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
10
                                                       700
                                     695
      GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA
Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu --
710 715 720 7
                                                                                    720 😽 🗀
                                                          715
                                710
      705
      CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG = 2772
      Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
                                                                735 348 X C
                                                     730
                           725
      ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu 740
745
750
      TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
20
                                                                    765
                755
                                           760
                                                                 2880
      GGA GGC AAG TCA
      Gly Gly Lys Ser
           770
      TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936
25
      (12) INFORMATION FOR SEQ ID NO:11:
             (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 3084 base pairs
                  (B) TYPE: nucleic acid
                  ·(C) strandedness:double
30
                    (D) TOPOLOGY:linear
             (ii) MOLECULE TYPE:genomic DNA
             (vi)ORIGINAL SOURCE:
                    (A) ORGANISM: Arthrobacter sp.
                    (B) INDIVIDUAL ISOLATE: Q36 (FERM BP-4316).
                    (A) NAME/KEY:5'UTR
             (ix) FEATURE:
                    (B) LOCATION: 1..677
                    (C) IDENTIFICATION METHOD: E-
                    (A) NAME/KEY: mat, peptide
                    (B) LOCATION: 678..3002
                    (C) IDENTIFICATION METHOD:S
                    (A) NAME/KEY: 3'UTR
                    (B) LOCATION: 3003..3073
                    (C) IDENTIFICATION METHOD: E
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
      GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG
      GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG
                                                                                              180
      CCGGACGAAT ACGCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC
TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT
CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA
                                                                                              240
                                                                                              300
       CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG
                                                                                              420
      GCCAAGACGA AGAAGCCGC CGCTGACCGC GCCGCTGACCC GCCGGTTGCT
GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG
CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCAGCCG
                                                                                              480
                                                                                              540
                                                                                              600
       GCGGAAAAGC CGGCGCGAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG
                                                                                              660
       CCCGCTGGGG AGGACGC
                                                                                              677
       ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC
      Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
```

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10
      ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
                   20
                                          25
      GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC
                                                                                 821
      Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
                                                            45
                                      40
      GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC
                                                                                 869
      Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
           50
                                 55
                                                       60
      GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC
                                                                                 917
      Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
      GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG
                                                                                 965
15
      Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
                        85
                                              90
      ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTC CAAG GAG GGA CGC
      Thr Pro Ala Gln Asn Pro Trp Trp Ser Leu Leu Lys Glu Gly Arg
      CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
                   100
                                                                110
      Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
20
                                                            125
               115
                                     120
      GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Leu Asp Gln
                                 135
      CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG - 1157
      Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro -
                            150
                                                   155
      CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC
                                                                               -1205
      Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
                        165
                                              170
                                                                    175
      GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG
                                                                                1253 -
      Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
30
                   180
                                          185
                                                              190 ·
      CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC
                                                                                1301
      Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
                                     200
                                                         - - 205
      GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC
                                                                                1349
      Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
35
                              - 215
      TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC
                                                                                1397
      Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
                            230
                                                   235
                                                                         240
                                                                                1445
      GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC
      Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
                        245
                                              250
40
      GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG
                                                                                1493
      Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
                                                                270
                   260
                                          265
      CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
                                     280
                                                            285
      GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu
                                 295
                                                       300
      GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG
                                                                                1637
      Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln 305 310 315
50
      GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC
                                                                                1685
      Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
                        325
                                                                     335
                                              330
      TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT
                                                                                1733
      Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
                   340
                                          345
```

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TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
                                    360
              355
     CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG
                                                                               1829
     Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
                                375
                                                      380
     GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC
                                                                               1877
     Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
10
                           390
                                                  395
     CAG GCT CTG CAG CCG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG
     Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
                                              410
                       405
     CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC
     Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
15
                                                               430
                                         425
                  420
     ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
              435
                                     440
     GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 12 2069
     Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
                                455
                                                      460
          450
     CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC
     Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
                            470
                                                  475
                                                                        480
     ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC
     Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
25
                                              490
                       485
     ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC
     Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
                                                               510
                  500
                                         505
     GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG
                                                                               2261
     Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
                                     520
                                                           525
     GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
                                                                               2309
                                                      540
                                535
     GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
                                                                               2357
                                                  555
                            550
     545
     CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG
                                                                               2405
     Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
                       565
                                              570
     TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC
                                                                               2453
     Phe Asp Asn Pro Ala Val Glu Ala Glu Val Glu Ala Leu Val Glu Leu
                                         585
                                                               590
                   580
     CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG
                                                                               2501
     Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
                                     600
              595
     CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG
     Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
                                                      620
                                615
          610
     GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC
                                                                               2597
     Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
                            630
                                                  635
     GAC CGC CGC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG
                                                                               2645
     Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
                                              650
                       645
     TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG
                                                                               2693
50
     Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
                                                               670
                   660
                                         665
     CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC
                                                                               2741
     Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
                                                           685
                                     680
     CTG GCC AGC GGG CCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC
```

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Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
           690
                                  695
                                                         700
      ACC GCG GCG GCG GCT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
                                                                                  2837
      705.
                             710
                                                    715
      GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC
                                                                                  2885
      Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
                         725
                                                730
                                                                      735
10
      ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
                    740
                                           745
                                                                  750
      GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG
                                                                                  2981
      Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
                755
                                     760
15
      CCG CAG ACA GGA GGA GAG TCA
                                                                                  3002
      Pro Gln Thr Gly Gly Glu Ser
           770
      TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062
      TCTGGGCGCC C
20
       (13) INFORMATION FOR SEQ ID NO:12:
             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 20
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: peptide
25
             (v) FRAGMENT TYPE: N-terminal fragment.
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
      Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
                         5
      Leu Phe Asp
30
                20
       (14) INFORMATION FOR SEQ ID NO:13:
             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 20
35
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: peptide
             (v) FRAGMENT TYPE: N-terminal fragment
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
      Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
                                                10
      Leu Phe Asp
                20
       (15) INFORMATION FOR SEQ ID NO:14:
45
            (i) SEQUENCE CHARACTERISTICS :
                  (A) LENGTH: 21
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE:peptide
             (v) FRAGMENT TYPE: internal fragment
50
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
      Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val Ile Ala Glu Val Ala Pro
                                                10
      Glu Trp Glu Lys
               20
55
```

```
(16) INFORMATION FOR SEQ ID NO:15:
              (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 21
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
              (ii) MOLECULE TYPE:peptide
              (v) FRAGMENT TYPE: internal fragment
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
10
       Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
                                                   10
                                                                          15
       Phe Trp Asp Arg
                 20
15
        (17) INFORMATION FOR SEQ ID NO:16:
              (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 20
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
20
              (ii) MOLECULE TYPE: peptide
              (v) FRAGMENT TYPE: internal fragment
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
       Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
25
       Phe Trp Asp
                 20
        (18) INFORMATION FOR SEQ ID NO:17:
             (i) SEQUENCE CHARACTERISTICS:
30
                   (A) LENGTH: 20
                   (B) TYPE: amino acid
                   (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE:peptide
             (v) FRAGMENT TYPE: internal fragment
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
35
       Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala Phe Asp
                                                                          Trp Asp Leu
                                                  10
                                                                          15
       Ala Gly Gly
                 20
40
    Claims
        A DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end
        unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.
        The DNA as claimed in claim 1, wherein said enzyme has the following physicochemical properties:
          (1) Molecular weight
          About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PA-
          (2) Isoelectric point (pl)
55
          About 3.6-4.6 on isoelectrophoresis.
```

The DNA as claimed in claim 1, wherein said enzyme has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and

homologous amino acid sequences to thes amino acid sequences:

5	SEQ ID NO:2									477							
	Met	Arg	Thr	Pro	Ala	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Arg	Gly	Phe	Thr
	1				5			-		10					15		
10	Leu	Phe	Asp	Ala	Ala	Glu	Thr	Val	Pro	Tyr	Leu	Lys	Ser	Leu	Gly	Val	Asp
			20					25					30				
	Trp	Ile	Tyr	Leu	Ser	Pro	Ile	Leu	Lys	Ala	Glu	Ser	Gly	Ser	Asp	His	Gly
15	35					40				1	45					50	
	Tyr	Asp	Val	Thr	Asp	Pro	Ala	Val	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55					60	:. ·	•	. ;	•	65 .			
20	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Gly	Ala	Gly	Met	Gly	Val	Leu
								•	- 1				•		•		

5			70					75					80					85
		Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Ser	Pro	Pro	Gln	· Asn	Pro
				٠, د		90					95					100		
0		Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gly	Ser	Pro	Tyr	Ala	Val	Ala
		· .		105					110					115			•	
15		Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu
3		120					125					130	-			٠	135	
		Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg
20					140					145				. :	150	- ;;	a ;	
.0		Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp
			155					160					165		٠		· · · .	170
25		Ser	Pro	Gln	Asp	Val	His	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	GLy	Trp	Arg
						175			•		180					185		
		Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
30				190				•	195					200	٠.			
		Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
2		205					210					215				.:	220	:3 :
35		Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
					225		. :			230	٠.				235	·. "	•	.!?
		Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
<del>1</del> 0			240	e.,				245					250					255
		Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glü	Gln
						260				٠	265	,		,	-	270		
<b>45</b>		Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
				275					280	٠				285				
		Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	qeA	Arg
50		290		- ,2			295					300					305	•
,	. :	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	Asp	Met	Ile
					310					315					320			

20

35

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_																	
5	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Lei
		325					330	٠				335			,		340
40	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
10	• • •	×		·: :	345				: .	350	•			7.4	355	•	
	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Тут
15		٠.	360		•			365	•	<b></b>			370		-		
,5	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	Ala	Cys	Asp	Leu	Ala	Ala	Arg
	375					380		• •			385					390	
20	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
		٠		395	Y .	<u>٠</u>	. •	• .	400	•				405	•	. :	-
	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln					
25		410					415			٠		420	•			ব হড়	425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
		-		÷	430		į	•	٠.	435	-				440	. :	
30	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
		٠	:445	:	•	•		450					455				
	Glu	Phe -	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
35	460	,			-	465					470		•			475	
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480					485					490	•		
40	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg
		495			·		500			·.		505					510
	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp
45			٠.	•	515	•				520				•	525		
•	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr
		¥ .	530				×*	535					540		· ·		
50		Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545					550		•			555					560	
	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
55				-													

5				565	5				570	)				575	5		
	Asn	Pro	Glu	ı Val	l Arg	, Ala	Glu	. Leu	Glu	. Ala	Leu	ı Val	Gly	Lei	ı Leı	ı Ala	a Pro
		580					585					590					59:
10	His	Gly	Ala	Ser	Asn	. Ser	Leu	Ala	Ala	Lys	Leu	. Val	Gln	Leu	ı Thr	: Met	: Pro
					600					605					610		
	Gly	Val	Pro	) Asp	Val	. Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arc	. Ser	Leu	ı Thi
15			615					620				_	625				
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu			Ara	Ala	יום.ל ו
	630					635					640		3		9		
20	Asp	:. Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser		Gln	Asn	Glu	- 645	
				650		_		. •	655				<b>U</b>	660		עדם	, Agi
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala		Ara	Leu	Ara	Ara			Pro	G1.,
25		665		•			670			5		675	9	11011	n.g	110	680
	Leu	Phe	Thr	Gly	Tyr	Arg		Val	His	Ala	Arg		Pro	Δla	<b>11</b> 2	G] 17	
		•		-	685					690		027		niu	695	GLY	urs
30	Leu	Val	Ala	Phe		Arg	Glv	Ala	Glv		Val	I.au	Ala	T.O.		Ψb.••	3
			700			J		705	1	1		204	710	Leu		1111	Arg
	Leu	Pro	Tyr	Glv	Leu	Glu	Gln		-GTv	Gl w	Trp	X =		mь		• <u>`</u>	<b>0</b> 3
35	715		4	2		720	· ·	JUL	OL,	GLY	725	ALG	ASP	THE	ATS		GIU
	Leu	Glu	Ala	λla	Met	-	Asn	Glu	T.o.u	<b>ም</b> ኤ ~	Gly	Com.	mb	Dha	. 01	730	<b>41</b>
			-	735			sp	Jiu	740	1111	GIY	ser	TAT		GTÀ	Pro	GLY
40	Pro	Ala	Ala		Ser	Glu	Val	Pho		<b>31</b> ~	Tyr			745	_	_	
٠.		750				014	755		ALG	vra	IĂT		vaı	ATS	ren	Leu	
			Thr	ឲាម	Gly	Luc					•	760			•		765
45 ·				017	770	БyS	261			r				٠.			
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~	SEQ :	ID N	0:4						٠		. ,						- '
55				Pro	Val -	Sa~ !	Th∽ '	T	N	•	<b>01</b>			-	<b>-</b> 1		
ş	Met 1	· y	~***		va. 5	GET.	IIIE .	ryr .			GIN	ile	Arg			Phe	Thr
	•				J					10				•	15		

5	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	Val	Asp
			20	•				25					30		•	· · ·	
	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gly
10	35			-		40				•	45					50	
	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55				·	60					65			
15	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Leu
		70					75					80					85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
20					90				•	95					100	*	
	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
		,	105	,				110			٠		115			•	
25	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu
	120	٠	•			125	- ;				130					135	
	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
30	<b>.</b> .		-	140					145			•		150			
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
		155					160					165					170
35	Ala	Pro	Arg	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
					175	•				180					185		٠.
40	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
40			190				•	195	•				200				
	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Alà	His	Gln	Glu
45	205				·.	210					215					220	
	Val	Val	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225		٠			230					235			
50	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	туг	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240				•	245					250					255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln

5					260	)				265	i				270		
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275	i				280	1				285				
10	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	290			-		295					300			٠,	•	305	
	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Įlle
15				310					315					320	;; ;;		
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325	٠				330			•		335	÷		· ·	a Inte	ૂ340
20	Arg	Leu	Ala	Arg	Leu	.Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
		٠.			345					350					355 :		
25	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Tyr
			360		. :			365				-	370				
	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg
30	375					380					385			-		390	
	Arg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
•		Α.		395			•		400					405		e vo	•
35	Asp		Asp	Leu	Glu	Leu		Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
•		410	•				415					420			i i s	•	
	Met	Ala	Lys	Gly		Glu	Asp	Thr	Ala		Phe	Arg	Tyr	Asn	Arg	Leu	Gly
40	_,				430			•		435			á		440	:	
	Thr	Leu		Glu	Val	GLY	Ala		Pro	Thr	Glu	Phe		Val	Glu	Pro	Asp
	<b>61</b>	<b>n</b> t .	445			_		450					455			**	
45		hue	HIS	ATS	Arg			Arg	Arg	Gln		Glu	Leu	Pro	Leu		Met
	460	Mb	<b>7</b>	C		465			_	_	470		•			475	
	THE	THE	Leu		THE	HIS	Asp	Thr		Arg	Ser	Glu	Asp		Arg	Ala	Arg
50	T1-	Ca	****	480		<b>61</b>	••-•		485	_		•		490		P	
	тте				ser			Ala ·	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	
		495	••	4			500					505					510

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5	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
					515					520					525	•	•
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
10	,		530			•		535					540		<b>,</b> ,		
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
	545					550					555					560	
15	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe .	Asp
				565	•				570				•	575		46.75	
20	Asn	Pro.	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
20	• • • • • • • • • • • • • • • • • • • •	580	٠٠.				585			•		590				±' .	595
	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
25	• *	٠٠.			600					605				٠	610	·, •	. 1
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
			615	•	,	•	٠.	620		•		•	625	•			Ŧ.
30	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	Asp	Arg	Arg	Ala	Ala	Leu
,	630			•		635					640	•				645	•
	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr
35				650			<u>.</u>		655		··			660			
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asp	Arg	Pro	
		665					670					675					680
40	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala		His
					685					690				•	695		
•	Leu	Leu	Ala	Phe	Asp	Arg	Gly	Thr	Ala	Ala	Ala	Pro			Leu	Thr	
45			700			•		705					710		-		: -
	Ala	Thr	Arg	Leu	Pro	Туг	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg		
	715					720			,:		725	•				. 730 ·.	
50	Ala	Val	Glu	Leu	ı Asr	Thr	Ala	Met	Lys	ysb	Glu	Leu	Thr		Ala	Gly	Phe
		-		735					740					745		•	
	Glý	Pro	Gly	Ala	val	. Lys	: Ile	Ala	ask i	Ile	Phe	Arg	Ser	Phe	Pro	Val	. Ala

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750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

770 775

4. The DNA as claimed in claim 1, which has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

SEQ ID NO:1

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ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT :: 60 GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC 1120 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180 GACCCGGAGC GCGGCGGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240 GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGCAG 300 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG -660 GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080 ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200

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5	CAGCTGCTGC	AGCCGCTGCT	GCTGGATACC	GACCTCGAGA	TTTCCCGCAG	GTTCCAGCAG	1260
	ACCTCGGGAA	TGGTCATGGC	CAAAGGCGTG	GAGGACACCG	CGTTCTTCCG	CTACAACCGG	1320
	CTGGGAACGC	TCACCGAGGT	GGGCGCCGAC	CCCACCGAGT	TCTCGCTGGA	ACCGGAGGAG	
10	TTTCACGTCC	GGATGGCCCG	CCGGCAGGCC	GAACTCCCGC	TCTCCATGAC	CACCCTGAGC	1440
	ACGCACGACA	CCAAGCGCAG	CGAGGACACC	CGGGCCCGGA	TCTCGGTGAT	CGCCGAGGTC	1500
	GCGCCTGAAT	GGGAAAAGGC	CCTGGACAGG	CTGAACACCC	TCGCTCCGCT	GCCGGACGGC	1560
15	CCGCTCTCCA	CGCTGCTCTG	GCAGGCGATT	GCGGGGGCAT	GGCCGGCCAG	CCGGGAACGC	1620
	CTTCAGTCCT	ACGCCCTGAA	AGCGGCGCGC	GAAGCCGGGA	ACTCGACCAG	CTGGACCGAT	1680
	CCGGACCCGG	CATTCGAGGA	GGCACTTTCC	GCCGTCGTCG	ACTCCGCCTT	CGACAATCCG	1740
20	GAGGTGCGTG	CGGAACTTGA	GCCCTGGTG	GGCCTCCTTG	CGCCGCACGG	TGCGTCCAAC	1800
	TEGETEGEGG	CAAAGCTTGT	CCAGCTGACC	ATGCCGGGCG	TTCCGGACGT	GTACCAGGGC	1860
	ACCGAGTTCT	GGGACAGGTC	GCTGACCGAT	CCGGACAACC	GGCGCCCCTT	CAGCTTCGCC	1920
25	GAACGGATTA	GGGCCTTGGA	CCAGTTGGAC	GCCGGCCACC	GTCCGGACTC	CTTCCAGGAC	1980
	GAGGCGGTCA	AGCTGCTGGT	CACCTCGAGG	GCGCTGCGGC	TGCGGCGGAA	CCGGCCCGAG	2040
	CTCTTCACCG.	GCTACCGCCC	CGTGCATGCC	AGGGCCCCG	CCGCCGGGCA	CCTGGTGGCG	2100
30	TTCGACCGCG	GCGCCGGGG	AGTGCTGGCG	CTTGCCACCC	GGCTCCCCTA	CGGGCTGGAA	2160
	CAGTCGGGCG	GCTGGCGGGA	CACCGCCGTC	GAGCTTGAAG	CCGCCATGAC	GGACGAACTG	2220
٠.	ACCGGCTCCA	CTTTCGGGCC	GGGACCGGCG	GCGCTGTCAG	AAGTCTTCCG	GGGCTACCCG	2280
35	GTGGCCTTGT	TGGTCCCCGC	GACAGGAGGC	AAGTCA			2316

SEQ	ID	NO	:3
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AT	GAGAACGC	CAGTCTCCAC	GTACAGGCTG	CAGATCAGGA	AGGGATTCAC	ACTCTTCGAC	60
GC	GGCCAAAA	CCGTTCCGTA	CCTGCACTCG	CTCGGCGTCG	ACTGGGTCTA	CCTTTCTCCG	.120
GT	CCTGACTG	CCGAGCAGGG	CTCCGACCAC	GGGTACGACG	TCACCGATCC	CTCCGCCGTC	180
GA	CCCCGAAC	GCGGCGGGCC	GGAGGGCCTC	GCGGCGGTTT	CCAAGGCGGC	cccccccc	240
GG	CATGGGCG	TGCTGATCGA	CATCGTGCCC	AACCACGTGG	GCGTCGCGAC	GCCGGCGCAG	300
AA	CCCCTGGT	GGTGGTCGCT	GCTCAAGGAG	GGACGCCAGT	CCCGTTACGC	GGAGGCGTTC	360
GA	CGTCGATT	GGGACCTCGC	CGGGGGACGC	ATCCGGCTGC	CGGTGCTCGG	CAGCGACGAT	420
GA	CCTCGACC	AGCTCGAAAT	CAGGGACGGG	GAGCTGCGGT	ACTACGACCA	CCGATTCCCG.	480

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CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCGC 600 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900 CAGGAACCGC TGGACCGCCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140 GTCCTGAAGG AGCCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380 TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620 CTGCAGTACT ACGCGCTGAA GGCCGCGCT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680 CCGGCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040 CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100 TTCGACCGCG GCACCGCGCC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220

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# GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

5. The DNA as claimed in claim 4, wherein one or more bases in SEQ ID NO:1 or 3 are replaced with other bases by means of degeneracy of genetic code without alternating the amino acid sequence of the following SEQ ID NO:2 or 4:

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	SEQ	ID	NO:2						•								
15	Met	Arg	Thr	Pro	Ala	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Arg	Gly	Phe	Thr
	1				5					10					15		
	Leu	Phe	Asp	Ala	Ala	Glu	Thr	Val	Pro	Туг	Leu	Lys	Ser	Leu	Gly	Val	Asp
20			20					25					30			,	
	Trp	Ile	Tyr	Leu	Ser	Pro	Ile	Leu	Lys	Ala	Glu	Ser	Gly	Ser	Asp	His	Gly
	35			•		40		٠			45					50	
25	Tyr	Asp	Val	Thr	Asp	Pro	Ala	Val	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55			ĵ		60					65			
	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Gly	Ala	Gly	Met	Gly	Val	Leu
30		70					75		•		•	80			. '		85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Ser	Pro	Pro	Gln	Asn	Pro
				_ : .	90					95					-100		
35	Trp	Trp	Trp	Ser	Leu	Leu	Lys	G1u	Gly	Arg	Gly	Ser	Pro	Tyr	Ala	Val	Ala
21.			105					110					115				
	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu
40	120	,		•		125	,				130			,		135	
	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg
45				140				•	145	•			1	.50		*	٠.
₩	Tyr	Tyr	qeA	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp
-		155					160					165					170
50	Ser	Pro	Gln	Asp	Val	His	Gly	Arg	Gln	His	Тут	Glu	Leu	Ile	Gly	Trp	Arg
J <b>u</b>					175	•				180		• .			185		

5	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
			190					195					200				
	Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glü	Ala	His	Gln	Glu
10	205					210					215					220	
	Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225					230					235	•	•••	
15	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240	÷				245					250					255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
20					260					265					270		
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
	٠		275				<i>:</i>	280					285				:.
25	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
	290					295					300				ė	305	
	Leu	Asp	Aĺa	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	Asp	Met	Ile
30				310					315					320		,.	
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
35	,	325			- 0		330					335		**			340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
					345					350					355		
40	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
			360					365				•	370				
	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	Ala	Cys	Ąsp	Leu	Ala	Ala	Arg
45	375					380					385			٠		390	
	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
				395					400					405			
50	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410				٠	415				•	420	٠	, -			425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly

5					430	)				435	i				440	).	
	Thr	Let	I Thi	Glu	ı Val	. Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Gl
			445	5				450	1				455	į		•	
10	Glu	Phe	His	: Val	. Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460					465					470					475	
	Thr	Thr	Leu	. Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
15				480					485					490	)	,	
	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg
		495	i				500					505				ا يا	510
20	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp
					515					520	i.				525		
25	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Gļlu	Arg	Leu	Gln	Ser	Tyr
25			530					535					540			,	
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
30	545		-			550					555					560	
	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
	-			565					570					575			
35	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
		580					585	•				590					595
	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
40					600		, ,			605			-		610		
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
			615			•		620			٠.		625		•		
45	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
	630	,				635	•				640				•	645	:
	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Gľu	Ala	Val
50				650					655		*			660			
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
		665					670					675				٠,	680

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	Leu	Phe	Thr	Gly		Arg	Pro	Val	His		Arg	Gly	Pro	Ala		Gly	His	
5					685					690					695			
	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg	
			700					705					710					
10	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu	
	715					720					725					730		
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly	
15				735					740					745				
	Pro	λla	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Val	
		750					755					760	•				765	
20	Pro	Ala	Thr	Gly	Gly	Lys	Ser								- :			
					770													
	v																	
25																		
							i	į.										
			-		•													
30		ID 1								•	. :			_				
30	Met			Pro		Ser	Thr	Tyr	Arg		Gln	Ile	Arg	Lys		Phe	Thr	
30	Met 1	Arg	Thr		5			•		10					15			
<b>30</b>	Met 1	Arg	Thr		5	Ser <u>L</u> ys		Val		10			Ser		15			
	Met 1 Leu	Arg Phe	Thr Asp	Ála	5 Ala	Lys	Thr	Val	Pro	10 Tyr	Leu	His	Ser 30	Leu	15 Gly	Val	Asp	
	Met 1 Leu	Arg Phe	Thr Asp	Ála	5 Ala		Thr	Val	Pro	10 Tyr	Leu Glu	His	Ser 30	Leu	15 Gly	Val	Asp	
	Met  1  Leu  Trp  35	Arg Phe Val	Thr Asp 20 Tyr	Ala Leu	5 Ala Ser	Lys Pro 40	Thr.	Val 25 Leu	Pro Thr	10 Tyr Ala	Leu Glu 45	His Gln	Ser 30 Gly	Leu Ser	15 Gly Asp	Val His 50	Asp	
<b>35</b>	Met  1  Leu  Trp  35	Arg Phe Val	Thr Asp 20 Tyr	Ala Leu	5 Ala Ser	Lys Pro	Thr.	Val 25 Leu	Pro Thr	10 Tyr Ala	Leu Glu 45	His Gln	Ser 30 Gly	Leu Ser	15 Gly Asp	Val His 50	Asp	
<b>35</b>	Met  Leu  Trp  35  Tyr	Arg Phe Val	Thr Asp 20 Tyr	Ala Leu Thr	Ala Ser Asp	Lys Pro 40 Pro	Thr. Val	Val 25 Leu Ala	Pro Thr Val	10 Tyr Ala Asp	Leu Glu 45 Pro	His Gln Glu	Ser 30 Gly Arg	Leu Ser Gly 65	Gly Asp Gly	Val His 50 Pro	Asp Gly Glu	
<b>35</b>	Met  Leu  Trp  35  Tyr	Arg Phe Val	Thr Asp 20 Tyr	Ala Leu Thr	Ala Ser Asp	Lys Pro 40	Thr. Val	Val 25 Leu Ala	Pro Thr Val	10 Tyr Ala Asp	Leu Glu 45 Pro	His Gln Glu Ala	Ser 30 Gly Arg	Leu Ser Gly 65	Gly Asp Gly	Val His 50 Pro	Asp Gly Glu Leu	
<b>35</b>	Met  Leu  Trp  35  Tyr	Arg Phe Val Asp Leu 70	Thr Asp 20 Tyr Val	Ala Leu Thr 55 Ala	Ser Asp	Lys Pro 40 Pro	Thr Val Ser Lys 75	Val 25 Leu Ala	Pro Thr Val 60 Ala	10 Tyr Ala Asp	Leu Glu 45 Pro	His Gln Glu Ala 80	Ser 30 Gly Arg	Leu Ser Gly 65 Met	Gly Asp Gly	Val His 50 Pro Val	Asp Gly Glu Leu 85	
35 40 45	Met  Leu  Trp  35  Tyr	Arg Phe Val Asp Leu 70	Thr Asp 20 Tyr Val	Ala Leu Thr 55 Ala	Ser Asp	Lys Pro 40 Pro	Thr Val Ser Lys 75	Val 25 Leu Ala	Pro Thr Val 60 Ala	10 Tyr Ala Asp Arg	Leu Glu 45 Pro	His Gln Glu Ala 80	Ser 30 Gly Arg	Leu Ser Gly 65 Met	Gly Asp Gly Gly	Val His 50 Pro Val	Asp Gly Glu Leu 85	
<b>35</b>	Met  1  Leu  Trp  35  Tyr  Gly	Phe Val Asp Leu 70 Asp	Thr Asp 20 Tyr Val Ala	Ala Leu Thr 55 Ala	5 Ala Ser Asp Val Pro	Lys Pro 40 Pro Ser	Thr Val Ser Lys 75	Val 25 Leu Ala Ala	Pro Thr Val 60 Ala	10 Tyr Ala Asp Arg Val 95	Glu 45 Pro Ala	His Gln Glu Ala 80 Thr	Ser 30 Gly Arg Gly	Leu Ser Gly 65 Met	Gly Gly Gln 100	Val His 50 Pro Val	Asp Gly Glu Leu 85 Pro	
35 40 45	Met  1  Leu  Trp  35  Tyr  Gly	Phe Val Asp Leu 70 Asp	Thr Asp 20 Tyr Val Ala	Ala Leu Thr 55 Ala	5 Ala Ser Asp Val Pro	Lys Pro 40 Pro	Thr Val Ser Lys 75	Val 25 Leu Ala Ala	Pro Thr Val 60 Ala	10 Tyr Ala Asp Arg Val 95	Glu 45 Pro Ala	His Gln Glu Ala 80 Thr	Ser 30 Gly Arg Gly Pro	Leu Ser Gly 65 Met	Gly Gly Gln 100	Val His 50 Pro Val	Asp Gly Glu Leu 85 Pro	
35 40 45	Met  Leu  Trp  35  Tyr  Gly  Ile	Arg Phe Val Asp Leu 70 Asp	Thr Asp 20 Tyr Val Ala Ile Trp 105	Ala Leu Thr 55 Ala Val	5 Ala Ser Asp Val Pro 90 Leu	Lys Pro 40 Pro Ser	Thr Val Ser Lys 75 His	Val 25 Leu Ala Ala Val Glu 110	Pro Thr Val 60 Ala Gly	10 Tyr Ala Asp Arg Val 95 Arg	Glu 45 Pro Ala Ala	His Gln Glu Ala 80 Thr	Ser 30 Gly Arg Gly Pro Arg 115	Leu Ser Gly 65 Met Ala	15 Gly Asp Gly Gln 100 Ala	Val His 50 Pro Val Asn	Asp Gly Glu Leu 85 Pro	

5	120					125					130					135	
	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
	,			140					145			•		150			
10	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
		155					160					165	-		·		170
	Ala	Pro	Arg	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
15					175					180				• •	,185	is +.	:*1
	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
			190					195					200	· · ·		<b>g.,</b> •.	
20	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala.	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
	205					210		•.			215				:	220	
25	Val	Val	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
25				225					230				. •	235			
	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
30		240	•				245				٠,	250	:			٠.	255
•	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
					260					265				٠	270		
35	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275					280					285			Y 4	.,:_
	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
40	290	•				295					300					305	
	Leu.	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
				310					315		ı		-	320			
45	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325					330			•		335		•			340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
<b>50</b>					345					350				٠	355		
	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Tyr
	•		360					365					370				

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5	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg
	375					380					385				·· .	390	
	Arg	Arg	Pro	Ġlu	Leu	Asp	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
10				395					400	ajir.		÷	٠	405		٠.	. **
	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410		•			415				•	420			79		425
15	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
					430					435				~ ·	440		
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp
20			445					450				D I	455	• • •			-
	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460					465					470		•			475	
25	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480			j		485	. •		.,		490	:	7 :	
	Ile	Ser	Vál	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
30		495	•				500			•		505	٠				510
	Leu	Arg	qsA	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
35				•	515					520					525		
<b></b>	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
			530					535	•				540	٠.	,		
40	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
	545					550					555					560	:
	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
45				565					570	•		:		575			
e'	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
		580					585		•			590					595
50	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
					600					605	: '	× , ,	. 10		610		
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala 630 635 640  Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu 650 655 660	645 Arg Thr
Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu	Arg Thr
10	
650 655 660	Pro Glu
333	Pro Glu
Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg	
665 670 675	680
Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala	Gly His
685 690 695	
Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Pro Gly Ala Leu	Thr Leu
700 705 710	
Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg	Asp Thr
25 715 720 725	730
Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala	Gly Phe
735 740 745	
30 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro	Val Ala
750 755 760	765
Leu Leu Val Pro Gln Thr Gly Gly Glu Ser	
770 775	***

6. The DNA as claimed in claim 1, which has the base sequence as shown in the following SEQ ID NO:10 or 11:

### 45 SEQ ID NO:10:

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CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60

CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120

GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180

CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240

TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300

GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360

GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGCC 420

			•		
5	GAAGCCGGA	AA GAGAAGGCTC CCG	ACGAGGC GGCGGCGAAG	CCGGAAGAGG CTGCTTCCGA	480
	CGAGGCGGC	CG GCGAAGCCCG CGG	GGAAGGC AGCGGCCAAA	ACGGCCGGCA GGCGAGCGCC	540
	AGGCAAGCA	AG GGCGGGACGG GCT	rc	·	564
10	ATG AGG A	CA CCC GCC TCG A	CC TAC CGG CTG CAG	ATC AGG CGG GGT TTC	612
	Met Arg T	Thr Pro Ala Ser	Thr Tyr Arg Leu Gli	n Ile Arg Arg Gly Phe	
	1	5	10	15	
15	ACG CTG T	TT GAT GCC GCC G	AG ACC GTG CCC TAC	CTG AAG TCA CTC GGG	660
	Thr Leu P	Phe Asp Ala Ala (	Glu Thr Val Pro Tyr	r Leu Lys Ser Leu Gly	
	٠	20	25	30	
20	GTG GAC T	GG ATC TAC CTG T	CG CCC ATC CTG AAG	GCA GAG AGC GGC TCC	708
	Val Asp T	Trp Ile Tyr Leu S	Ser Pro Ile Leu Lys	s Ala Glu Ser Gly Ser	
	3	35	40	45	_
25	GAC CAC G	GC TAT GAC GTC A	CC GAT CCC GCC GTA	GTG GAC CCG GAG CGC	756
	Asp His G	Gly Tyr Asp Val	Thr Asp Pro Ala Va	l Val Asp Pro Glu Arg	
20	50		55 **	60	
30	GGC GGC C	CT GAA GGG CTG G	CC GCG GTG TCC AAG	GCG GCC CGC GGT GCC	804
	Gly Gly P	Pro Glu Gly Leu A	Ala Ala Val Ser Ly:	s Ala Ala Arg Gly Ala	
35	65	70	75	80	
				CAC GTG GGC GTG GCG	852
	Gly Met G	Gly Val Leu Ile	Asp Ile Val Pro Ası	n His Val Gly Val Ala	
40	•	85	90	95	
	•			CTC AAG GAA GGG CGC	900
	Ser Pro P	Pro Gln Asn Pro	Erp Trp Trp Ser Le	u Leu Lys Glu Gly Arg	
45		100	105	110	
		**		TGG GAC CTG GCG GGG	948
	•			o Trp Asp Leu Ala Gly	
<b>50</b> .			120	125	001
				GAC GAT CTG GAC CAG	996
	Gly Arg I	le Arg Ile Pro \	/al Leu Gly Ser Asp	p Asp Asp Leu Asp Gln	

5		130					135					140	,				
	CTC	GAA	ATC	AAG	GAC	GGC	GAG	CTG	CGG '	rac 1	rac G	AC C	AC C	GC T	TC C	CG.	104
	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	Arg	Phe	Pro	
10	145	. •	•			150					155					160	
	CTG	GCC	GAG	GGC	AGC	TAC	CGG	GAC	GGC	GAC 1	rcc c	CG C	AG G	AC G	TC C	AC	109
	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp	Ser	Pro	Gln	Asp	Val	His	
15					165					170					175	•	.,
	GGC	CGG	CAG	CAC	TAC	GAA	CTC	ATC	GGC '	rgg (	CGG C	GC G	CC G	AC A	AT G	4A	1140
	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Asp	Asn	G1u	•
20				180					185					190			
	CTG	AAC	TAC	CGC	CGG	TTC	TTC	GCG	GTG A	AAC A	ACG C	TC G	CC G	GC A	TC C	GG	1188
	Leu	Asn	Tyr	Arg	Ārg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gly	Ile	Arg	
25			195	e e				200					205	,		'	
	GTG	GAG	GTG	CCG	CCG	GTC	TTC	GAT	GAA (	GCG (	CAC C	AG G	AG G	TG G	TG CC	GC	1236
30	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu	Val	Val	Arg	
••		210					215					220			-	-; f .	
	TGG	TTC	CGT	GCG	GGG	CTC	GCC	GAC	GGG (	CTG C	GG A	TC G	AC C	AC C	CG G	AC <sub>f</sub> .	1284
35	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His	Pro	Asp	
-31 -	.225		- '	-		230					235					240	
	GGC	CTG	GCC	GAT	CCC	GAG	GGG	TAT	TTG A	AAG C	GG C	TC C	gt g	AG G	TC AC	C	1332
40	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val	Thr	
					245		,			250	****				255		
	GGG	GGC	GCG	TAC	CTG	CTC .	ATC (	GAA .	AAG A	TC C	TC G	AG C	CG G	GC G	AA CA	.G	1380
45	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln	
. ,	,	•		260					265	. •	•			270	*		٠,
	TTG	CCG	GCC	AGC	TTC	GAG '	rgc (	GAA (	GGC A	CC A	CC G	GC T	AC G	AC GO	CC CI	C	1428
50	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly.	Tyr	Asp	Ala	Leu	
			275					280					285				-
	GCG	GAT	GTC	GAC .	AGG	GTC 1	TTC (	STG (	GAC C	CG C	GG G	GA C	AG G	rg co	CG CT	G	1476

5	Ala	Asp	Val	qeA	Arg	Val	Phe	Val	Asp	Pro	Ãrg	Gly	Gln	Val	Pro	Leu	
		290		. •			295	•	•		- * *	300					
	GAC	CGT	CTG	GAC	GCA	CGG	CTG	CGC (	GGC (	GT G	ece c	cc c	CC G	AC T	AC G	AĢ	1524
10	Asp	Arg	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	•
	305			,		310					315		;			320	
	GAC	ATG	ATC	CGC	GGG	ACC	AAG (	CGC (	CGG 1	ATC A	CC G	AC G	GC A	TC C	TG C	AC	1572
15	Asp	Met	Ile	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	
		,			325			•		330	•				335		
	TCC	GAG	ATC	CTG	CGC	CTT	GCC .	AGG .	CTG (	STG C	CC G	AG C	AG A	CC G	GA A	TT	1.620
20	Ser	Glu	Ile	Leu	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	
		-		340					345				•	350	*		•
	CCC	GGG	GAG	GCG	GCC	GCG	GAT (	GCG 2	ATC (	SCG G	GAG A	TC A	TC G	CG G	CC T	rc	1668
25	Pro	Gly	Glu	Ala	Ala	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	
			355			• .		360					365				
20	CCG	GTC	TAC	CGG	TCC	TAT	CTT (	ccc (	GAG (	GC G	CG G	AG A	TC C	TG A	AG G	AG ·	1716
30	Pro	Val	Tyr	Arg	Ser	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	
		370			•		375					380			,	. 7,	
35	GCC	TGC	GAC	CTC	GCC	GCG	CGG /	AGG (	CGT (	CCG .G	AA C	TG G	GC C	AG A	CC G1	rc -	1764
	Ala	Суз	Asp	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	
	385					390			•		395					400	
40	CAG	CTG	CTG	CAG	CCG	CTG	CTG (	CTG (	GAT A	CC G	AC C	TC G	AG A	TT TO	cc ca	€C	1812
	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	
					405					410					415	. ,	
45	AGG	TTC	CAG	CAG	ACC	TCG	GGA 2	ATG (	STC A	TG G	CC A	AA G	GC G	TG G	AG GA	C	1860
٠.	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	
				420	•				425					430			
50						TAC		•									1908
	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
			435					440					445				

5	GCC	GAC	CCC	ACC	GAG	TTC	TCG	CTG	GAA (	CCG (	GAG G	GAG T	TT C	AC G	TC C	GĞ	1956
	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu	Glu	Phe	His	Val	Arg	Ī
		450			· ·		455		-			460	;				
10	ATG	GCC	CGC	CGG	CAG	GCC	GAA	CTC	CCG (	CTC 7	rcc a	TG A	CC A	cc c	TG A	GC	2004
	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	`
	465					470					475				: ;	480	<u>.</u> 2
15	ACG	CAC	GAC	ACC	AAG	CGC	AGC	GAG (	GAC A	ACC C	GG G	CC C	GG A	TC T	CG G	rG	2052
	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
	;	: 1, -	: •		485				٠	490					495	×47.	
20	ATC	GCC	GAG	GTC	GCG	CCT	GAA	TGG (	GAA A	AG G	CC C	TG G	AC A	GG C	TG A	AC	2100
	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg	Leu	Asn	
25	•	;	•	500		-			505					510		. • -	
25	ACC	CTC	GCT	CCG	CTG	CCG	GAC	GGC (	CCG C	TC T	CC A	CG CI	rg C	rc T	GG C	4G	2148
	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp	Gln	
30			515	· ·	<del>-</del>			520					525				
											AA C					•	2196
	Ala	- '		Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr	-1.4D
35		530			-		535			-		540	7 *-	•	ا المامينية 1 المعروف		÷
											CG A				•	• • • • • • • • • • • • • • • • • • • •	2244
		Leu	Lys	Ala	Ala		Glu	Ala	Gly	Asn	Ser	Thr :	Ser	Trp	Thr	Asp	
40	545	<b>~1 ~</b>				550					555					560	
											CC G				•		2292
	PIO	ASP	PIO	ATS		GIU	GIU	ATA			Ala	Val V	Val .	Asp		Ala	
45	<b>መ</b> ሞር	CAC	3 3 M	000	565	·				570					575		
·											AG GC						2340
	rne	vah		580	GIU	Val	Arg		•	Leu	Glu	Ala I	•		СТĀ	Leu	
50	C TO TO	: ccć i			COM .	300 -			585					590			
v											CG GC						2388
	neu	vrg	PLO	HIS	GTA	мтя	ser	Asn .	ser	Leu .	Ala	Ala I	Lys 1	Leu	Val	Gln	

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5	•		59 <sup>5</sup>		7.	.:	J.: 1.	600					605				
	CTG	ACC	ATG	CCG	GGC	GTT	CCG	GAC	GTG	TAC (	CAG (	GGC A	CC G	AG 1	TC T	GG <sup>.</sup>	2436
	Leu	Thr	Met	Pro	Gly	Val	Pro	Asp	Val	Туг	Gln	Gly	Thr	Glu	Phe	Trp	
0		610		200	,,,,,	• ;	615		<b>.</b>	. 3		620					
	GAC	AGG	TCG	CTG	ACC	GAT	CCG	GAC	AAC	CGG (	CGC (	CCC T	TC A	GC I	TC G	CC	2484
	Asp	Arg	Ser	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	
5	625				****	630		•			635					640	
	GAA	CGG	ATT	AGG	GCC	TTG	GAC	CAG	TTG	GAC (	SCC (	GC C	AC C	GT C	CG G	AC	2532
	Glu	_		_				Gln	_		Ala	Gly	His	Arg	Pro	Asp	
0	•	; • ·	: :)TL		645	e and			* %	650	• •			•	655	ىت الس¥لودان	
	TCC	TTC	CAG	GAC	GAG	GCG	GTC	AAG	CTG	CTG (	STC A	ACC T	CG A	.GG G	CG C	rg	2580
95	Ser	Phe	Gln	Asp	Glu	Ala	Val	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	٠
.5 ,	. " .	31.	_	660				_	665				•	670	,		
	CGG	CTG	CGG	CGG	AAC	CGG	CCC	GAG	CTC	TTC /	ACC (	GC T	AC C	GC C	CC G	rg	2628
BO	Arg			,	Asn	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	
	•		675					680		:			685			* .	
•	CAT	GCC	AGG	GGC	CCC	GCC	GCC	GGG	CAC	CTG (	GTG (	GCG T	TC G	AC C	GC G	GC.	2676
35	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His	Leu	Val	Ala	Phe	Asp	Arg	Gly	
-		690	•				695	·				700					
										•					TG G		2724
10	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	
	705					710					715					720	
			~ ·												CC A		2772
15	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	·	Glu	Leu	Glu	Ala	Ala	Met	•.
'	•			t;	725		٠,		*	730					735	٠.	 
- •				. 2											CG C		2820
50	Thr	Asp	Glu	s		Gly	Ser	Thr			Pro	Gly	Pro		Ala	Leu	
٠,	•	,		740					745					750			
	TCA	GAA	GTC	TTC	CGG	GCC	TAC	CCG	GTG (	GCC 1	TG I	TG G	TC C	CC G	CG A	CA	2868

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	Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr	
	755 760 765	
5	GGA GGC AAG TCA	2880
	Gly Gly Lys Ser	
	770	
10	TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC	2936
15		
20	SEQ ID NO:11	
	GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG	60
	GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG	120
25	GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG	180
	CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC	240
	TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT	300
30	CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA	360
	CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG	420
	GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT	480
35	GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG	540
	CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG	600
	GCGGAAAAGC CGGCGCGAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG	660
40	CCCGCTGGGG AGGACGC	677
	ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC	725
	Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe	*
45	1 10 15	
	ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC	773
	Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly	
50	20 25 30	
	GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC	821
	Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser	·
55	35 40 45	

5	GAC	CAC	GGG	TAC	GAC	GTC	ACC	GAT	ccc '	rcc (	GCC (	STC C	SAC C	cc e	AA C	:GC	869
	Asp	His	Gly	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	
		50					55		_			60				. *	
10	GGC	GGG	CCG	GAG	GGC	CTC	GCG	GCG	GTT '	rcc i	AAG C	SCG (	cc c	GC G	CC G	CG	917
	Gly	Gly	Pro	Glu	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	
	65		•			70					75					80	
15	GGC	ATG	GGC	GTG	CTG	ATC	GAC	ATC	GTG (	ccc /	AAC Ç	CAC C	STG G	GC G	TC G	CG	965
	Gly	Met	Gly	Val	Leu	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	
		,	÷		85					90					95	·	
20	ACG	CCG	GCG	CAG	AAC	CCC	TGG	TGG	TGG' '	rcg (	CTG (	CTC A	AG G	AG G	GA C	GC -	1013
-	Thr	Pro	Ala	Gln	Asn	Pro	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	
•	: '	. ()	• •	100	-		÷		105					110	•		
25	CAG	TCC	CGT	TAC	GCG	GAG	GCG	TTC	GAC (	GTC (	GAT 1	rgg d	AC C	TC G	CC G	GG	1061
	Gln	Ser	Arg	Tyr	Alá	Glu	Ala	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	
		• • • •	115		17			120					125			٠.	
30	GGA	,cec	ATC	CGG	ĊTG	CCG	GTG	CTC	GGC 2	AGC (	GAC (	SAT C	SAC C	TC G	AC C	AG	1109
	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asp	Leu	Asp	'Gln	
		130	- 3- -			. •	135	•				140	•	•	•		
35	CTC	GAA	ATC	AGG	GAC	GGG	GAG	CTG	CGG '	TAC '	TAC (	GAC C	CAC C	GA I	TC C	CG	1157
	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	Arg	Phe	Pro	
40	145					150	١				155					160	
40	CTC	GCC	GAG	GGA	ACC	TAC	GCC	GAA	GGC (	GAC	GCC (	CCG ·C	CGG G	AT G	TC C	CAC	1205
	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp	Ala	Pro	Arg	Asp	Val	His	
45					165					170	)				175	;	
	GCC	CGG	CAG	CAC	TAC	GAG	CTC	ATC	GGC	TGG (	cgc (	CGC (	CG G	AC A	AC G	AG	1253
	Ala	Arġ	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Asp	Asn	Glu	
50				180					185					190			
	CTG	AAC	TAC	CGC	CGC	TTT	TTC	GCG	GTG .	AAC .	ACG (	CTC (	GCC G	GC G	STC C	CGC	130
* *.	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gly	Val	Arg	

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58

5 .			195	:				200					20	5				
	GTG	GAA	ATC	ccc	GCC	GTC	TTC	GAC	GAG (	GCA (	CAC C	CAG (	GAG	GTG	GTG	CGC	1349	3
	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	G1:	ı Va	l Va	ıl A	cg	
10		210				Υ .	215		-			220					•	
	TGG	TTC	CGC	GAG	GAC	CTT	GCG	GAC	GGC (	CTG (	CGG <sub>,</sub> A	ATC (	GAC	CAC	CCG	GAC	1397	7
	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Ası	, Hi	s Pr	:o A:	sp	
15	225					230	•	· .			235			~, · .		24	40	
	GGC	CTC	GCT	GAC	ccc	GAG	GGG	TAC	CTG 2	AAG (	CGA C	TC (	CGG	GAA	GTC	ACC	1445	5
	Gly	Leu	Ala	. Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	g Gl	u. Va	.1Tl	ar.	
20					245		. :			250					25	5 /		
	GGC	GGC.	GCT	TAC	CTG	CTG	ATC	GAA	AAG A	ATC (	CTG G	ag (	CCG	GGG	GAG	CAG	1493	3
	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gl;	y Gl	u G	ln.	
25				.260				• :	265					27	0			
	CTG	CCC	GCC	AGC	TTC	GAG	TGT	GAA	GGC 1	ACC 2	ACA G	GC 1	rac	GAC	GCC	CTC	1541	L
	Leu	Pro	Ala	Ser	Phe	Glu	Суз	Glu	Gly	Thr	Thr	Gly	Туз	As	p Al	a Le	eu	
30			275					280					285	5				
*	GCC	GAC	GTC	GAC	CGG	GTT	CTC	GTG	GAC (	CCG (	CGC G	igc (	CAG	GAA	CCG	CTG	1589	)
·	Ala	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Glr	Gl	u Pr	o Le	eu -	
35		290					295					300		2.50			. 5.4	
	GAC	CGG	CTT	GAC	GCG	TCC	CTG	CGT	GGC. (	GC (	GAG C	cc c	SCC (	GAC	TAC	CAG	1637	7
40	Asp	Arg	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	a As	р Ту	r Gl	ln -	
•••	305					310					315					32	20	
	GAC	ATG	ATC	CGC	GGA.	ACC	AAG	CGC	CGG A	ATC A	ACC G	AC C	GT A	ATC	CTG	CAC	1685	5
45	Asp	Met	Ile	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gl	, Il	e Le	u Hi	is	
			**		. 325					330					33	5		
•	TCG	GAG	ATC	CTG	CCC	CTG	GCC	CGG	CTG C	STT C	CCG G	GC 0	FAC (	GCC .	AAC	GTT	1733	Ì
50	Ser	Glu	Ile	Leu	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	a As	n Va	1	
-			~~	340					345					350	0			
	TCA	ATC	GAC	GCC	GGA	GCC	GAC (	GCT (	CTC	SCC 0	SAA A	TC A	TC (	GCC	GCC	TTC	1781	

5	Ser	Ile	Asp	Ala	Gly	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	
	-		355					360					365	٠			
	CCG	GTC	TAC	CGC	ACC	TAC (	CTG (	ccg c	SAG G	GC G	CC G	AG G	TC C	TG A	AG G	AG	1829
10	Pro	Val	Tyr	Arg	Thr	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	
-		370	• ,,	·			375					380					
	GCG		GAG	CTT	GCC	GCG	CGT I	AGG (	cgg c	CG G	AA C	TC G	AC C	AG G	CC A	TC	1877
15														Gln			
	385	-4				390					395					400	
		GCT'	CTG	CAG	CCG	CTG ·	CTG (	CTG (	GAC A	ACG G	AC C	CTC G	AG C	TT G	cc c	GG	1925
20														Leu			
	: .				405				_	410					415		
	CGC	ጥጥር	CAG	CÄG			GGC .	ATG (	GTC A	ATG G	SCC 1	AAG G	GC G	TG G	AG G	AC	1973
25														Val			
				420			•	i	425					430		. : ;	* .
	እርር	GCG	ጥጥር			TAC	AAC	CGC	CTG (	GC 1	ACC (	CTC A	CG G	AA G	TG G	GC	2021
30														Glu			
	1111	ALU	435			-1-		440		•			445				
	ccc	GAC			GAG	ттс	GCC			CCG (	GAC (	GAG I	TC C	CAC G	cc c	GG	2069
35											10.00	- 11 -		His			
	VIG	450			0		455				•	460					
**.	CTC			ccc	CAG	GCC			CCG (	CTG 1	rcc i			CG C	TG A	GC	2117
40														Thr			
			ALG	, nra	المبد	470		. 200			475					480	
	465			» cic	220			GNG	GAC.	ארר (			AGG 2	\TT T	CG C	TC ·	2165
45														Ile			•
	Thr	HIS	Asp	Thi			Ser	GIU	, vah	490					495		
	<u>:</u>	ma			485		CAC	TICC	CAA			ጥጥር 1	AAC (	cee c			2213
50																	
	Ile	Ser	GIu			" ста	ASP	rrp			: ATE	, neu	, var	<b>Arg</b> 510			
				500	)				505	•	•			310	•		

<b>၁</b>				
_	GAC CTG GCC CCG CTG	CCG GAC GGC CCG C	IG TCC GCG CTG CTC TGG	CAG 2261
			Leu Ser Ala Leu Leu T	
10	515	520	525	
	GCC ATT GCC GGC GCC	TGG CCC GCC AGC CC	GG GAA CGC CTG CAG TAC	TAC 2309
			Arg Glu Arg Leu Gln Ty	
15	530	535	540	. ·. · -
	GCG CTG AAG GCC GCG	CGT GAA GCG GGG AA	C TCG ACC AAC TGG ACC	GAT 2357
			sn Ser Thr Asn Trp Th	
20		550	555	⊖. ઁ 560
	CCG GCC CCC GCG TTC (	GAG GAG AAG CTG AA	G GCC GCG GTC GAC GCC	GTG 2405
			ys Ala Ala Val Asp Al	
25	565	•	70 57	
	TTC GAC AAT CCC GCC G	TG CAG GCC GAG GT	G GAA GCC CTC GTC GAG	CTC 2453
	Phe Asp Asn Pro Ala	Val Gin Ala Glu V	al Glu Ala Leu Val Gl	u Leu
30	580	585	590	٠
	CTG GAG CCG TAC GGA G	CT TCG AAC TCC CTC	GCC GCC AAG CTC GTG	CAG 2501
	Leu Glu Pro Tyr Gly	Ala Ser Asn Ser Le	eu Ala Ala Lys Leu Val	l Gln
35	595	600	605	
			CAG GGC ACG GAG TTC	
	Leu Thr Met Pro Gly V	al Pro Asp Val Ty	r Gln Gly Thr Glu Phe	Trp
40	610	615	620	•
			CGG CCG TTC AGC TTC G	
		sp Pro Asp Asn Ar	g Arg Pro Phe Ser Phe	Asp
45		30	635	640
	GAC CGC CGC GCC GCG CT			
	Asp Arg Arg Ala Ala L	eu Glu Gln Leu As	p Ala Gly Asp Leu Pro	Ala
50	645	650	,,555	
	TCA TTT ACC GAT GAG CG			
	Ser Phe Thr Asp Glu A	rg Thr Lys Leu Leu	Val Thr Ser Arg Ala	Leu
55	χ.			•

5				660				,	665					670		٠ سرندن	
	CGG	CTG	CGC	CGG	GAC	CGT	CCG	GAG (	CTG 1	TTC A	CG C	GG I	'AC C	GG C	CG G	TC.	2741
	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	
0			675					680					685				
-	CTG	GCC	AGC	GGG	ccc	GCC	GCC	GGG (	CAC (	CTG C	TC C	CG T	TC G	AC C	GC G	сĊ	2789
	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His	Leu	Leu	Ala	Phe	Asp	Arg	Gly	
15		690					695					700					•
	ACC	GCG	GCG	GCG	CCG	GGT	GCA '	TTG I	ACC (	CTC G	CC A	cg c	GG C	TT C	CC T	AC	2837
	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu	Ala	Thr	Arg	Leu	Pro	Tyr	
20	705					710					715	•				720	• • •
	GGG	CTG	GAA	CAG	TCG	GGT	GGA '	TGG (	CGG (	SAC A	.cc g	CC G	TC G	AA C	TT A	AC .:	2885
	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu	Leu	Asn	
?5				·	725					730			٠.		735	·: .	. 1*1
	ACC	GCC	ATG	AAA	GAC	GAA	CTG 2	ACC (	GGT (	CC G	GC T	TC G	GA C	CG G	GG GG	CA	2933
••	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe	Gly	Pro	Gly	Ala	
<b>\$</b> 0	٠			740	-				745			52		750		-1-	
	GTG	AAG	ATC	GCC	GAC	ATC	TTC (	CGG 1	rcg 1	TC C	CC G	TT G	CG .C	TG C	rg gr	rg	2981
35	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala	Leu	Leu	Val	
			755				7	760				7	765				
	CCG	CAG	ACA	GGA	GGA	GAG	TCA										3002
<b>4</b> 0	Pro	Gln	Thr	Gly	Gly	Glu	Ser								-		
		770					775						•	•			-
	TGAC	GCAC	CAC C	TACC	CGCG	G GA	AGCC	GCGA	AACC	CGTC	CT G	GGCC	CCGC.	A CGC	TAC	BACG	3062
45	TCTG	GGC	cc c	:					•								3073
												•					2

- The DNA as claimed in claim 1, which is derived from a microorganism selected from the group consisting
  of those of the genera Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium and Terrabacter.
  - 8. A replicable recombinant DNA containing the DNA of claim 1 and a self-replicable vector.
  - 9. The r plicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having the following physicochemical properties:
    - (1) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PA-GE); and

(2) Isoelectric point (pl)

About 3.6-4.6 on isoelectrophoresis.

10. The replicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having an amino acid sequence selected from the group consisting of those as shown in SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous base sequences to these amino acid sequences:

10

SEQ ID NO:2

5

15

20

25

30

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
90 95 100

35

40

45

55

5	Tr	Tr	Tr	o Sei	r Lev	Leu	ı Lys	s Glu	Gl	, Arg	g Gly	, Ser	Pro	Ty	r Ala	a Val	L Ala
			105	5				110	)				115	5		e hai.ī.	
	Phe	Asg	va]	L Asg	Trp	Asp	Leu	ı Ala	Gl	, G13	, Arg	, Ile	Arc	; Ile	e Pro	Val	Leu
10	120					125					130					135	
	Gly	Ser	. Asr	) Asr	) Asp	Leu	Asp	Gln	Leu	ı Glu	ı Ile	Lys	Asp	Gly	, Glu	Leu	Arg
				140					145					150			
15	Туг	туг	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Туг	Arc	, Asp	Gly	Asp
		155					160				•	165					170
	Ser	Pro	Gln	Asp	. Val	His	Gly	Arg	Gln	His	Туг	Glu	Leu	Ile	Gly	Trp	Arg
20					175					180					185	:	·
	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
			190					195					200			;	::'
25	Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
	205					210	1.				215			•		220	
	Val	Val	Árg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
30				225					230					235		٠.	• .
	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240					245				-	250					255
35	Thr	Gly	Gly	Ala	TYT	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
					260				•	265					270		
40	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
~			275					280				٠,	285			•	
	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
45	290					295					300					305	•
75	Leu	qeA	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	qeA	Met	Ile
				310					315					320			•
50	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
50		325					330					335			·		340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala

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5					345					350	• •				355		
	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
	•		360					365					370		<u>.</u>	,	
10	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	Ala	Cys	Asp	Leu	Ala	Ala	Arg
	375					380					385	•	• .		: .	: 390	<i>:</i> .
	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
15 .			•	395					400		,			405	. '• • • •	•	-
	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410					415		٠	•	1	420	*		::	٠ <u>.</u> چ	425
20	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Тут	Asn	Arg	Leu	Gly
				•	430					435	•				440		•
25	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
25			445					450	•				455				
	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
30	460			٠		465	. ``		•		470			•	*. ·	475	•
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480					485	•				490	`- ••	- ·	* *
35	Ile	Ser	Val	Ile	Ala	<b>Gl</b> u	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu		Arg
		495	•				500					505				 	510
	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr			Trp
40					515					520		•			525		•
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr
			530					535					540				
45	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545					550					555					560	
	Asp	Pro	Ala	Phe	Glu	G1u	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
50				565					570				-	575			
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
		580				•	585					590			. :		595

5	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
					600					605					610		
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
10			615					620					625			ą.	
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
	630	,				635					640					645	
15	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Glu	Ala	Val
				650					655				•	660			,
	Lys	Leu	Leu	Val	Thr.	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
20		665					670					675			• •	<del></del> .	680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
					685		•			690					695	. : -2.	
25	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
			700		•		į	705					710	٠.	:		
	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu
<b>30</b>	715					720			٠		725				٠.	730	
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly
•	٠			735		. :	r		740					745			
35	Pro	Ala	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Val
		750			•		755	a.	. '			760					765
	Pro	Ala	Thr	Gly	Gly	Lys	Ser				,						
40					770			i									

	SEQ	ID I	NO : 4														,
5	Met	Arg	Thr	Pro	Val	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Lys	Gly	Phe	·Thr
	1				5					10					15		
	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	Val	Asp
10			20					25					30			•	
	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gly
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5	35					40					45					50·	
	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55					60					65			
10	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Leu
		70					75					80				-	85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
15					90					95					100		
	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
			105				•	110					115			-9	
20	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Île	Arg	Leu	Pro	Val	Leu
	120					125					130					135	
05	Gly	Ser	Asp	qaA	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
25				140					145		. •			150			
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
30		155	•				160					165					170
30	Ala	Pro	Arg	qzA	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
					175					180					185		
35	Arg	Ala	qeA	Asn	Glu	Leu	neA	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
			190					195				-	200				
	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
40	205					210				•	215					220	
	Val	Val	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225					230					235			
45	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240					245					250					255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
50					260				•	265					270		
٠	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275					280					285				

5	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	290				2. I.	295			<i>:</i> .		300				20	305	
	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
10				310			. 0		315					320			·.
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325					330					335					340
15	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
					345				. •	350				.10	355	.5 ··	· ''
	Ala	Asp	Ala	Leu	Ala	Glu	Ile.	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Tyr
20	•		360			•		365					370		······		
	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg
	375					380				٠	385					390	
25	Arg	Arg	Pro	Glu	Leu	yab	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
				395			i	. ,	400					405	•	•	
	Asp	Thr	Asp	Leu	Glu	Leu	Äla	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
30		410			,	٠.,	415					420		:	. 134	É.	425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asņ	Arg	Leu	Gly
35	:				430	-	, i			435			-1	tan j	440	uti ;	
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp
		•	445					450					455				•
40	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460					465					470					475	
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
45				480			-		485			. •		490	•		
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
		495					500					505					510
<b>50</b>	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	qeA	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
					515					520					525		
•	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr

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5			530					535				•	540			•	
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
	545			-		550			•		555					560	
10	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
	:::::::::::::::::::::::::::::::::::::::		•	565			-		570					575	٠	•	
	Asn	Pro	Ala	Val	Gĺn	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
15	· . •	580					585				•	590					595
	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
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20	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
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	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ąsp	Asp	Arg	Arg	Ala	Ala	Leu
25	630		•		• •	635					640				_ ` `	645	• !
	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr
30		•	7	650					655					660	•		
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Ļeu	Arg	Leu	Arg	Arg	Asp	Arg.	Pro	Glu
		665	,				670					675		,		36 - 36 3 - 3 3 - 3	680
35	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His
- •					685					690					695		
	Leu	Leu	Ala	Phe	Asp	Arg	Gly	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu
40			700					705					710	•	:		
	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr
	715					720		7.			725 ·					730	
45	Ala	Val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe
				735		٠			740					745			
	Gly	Pro	Gly	Ala	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	
50		750			,	-	755					760.					765
	Leu	Leu	Val	Pro	Gln	Thr	Gly	Gly	Glu	Ser					٠		•
					770		-			775					•		

11. The replicable recombinant DNA as claimed in claim 8, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to the se base sequences:

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#### SEQ ID NO:1

10 ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC 120 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180 15 GACCCGGAGC GCGGCGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240 GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGCAG 1300 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360 20 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540 25 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660 GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720 30 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 35 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080 4n ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320

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C'	rgggaacg	C TCAC	CGAGGT	GGGCGCCGAC	CCCACCGAGT	TCTCGCTGGA	ACCGGAGGAG	1380
T	rtcacgtc	C GGAT	GCCCG	CCGGCAGGCC	GAACTCCCGC	TCTCCATGAC	CACCCTGAGC	1440
A	CGCACGAC	A CCAA	GCGCAG	CGAGGACACC	CGGGCCCGGA	TCTCGGTGAT	CGCCGAGGTC	1500
G	CGCCTGAA	T GGGA	AAAGGC	CCTGGACAGG	CTGAACACCC	TCGCTCCGCT	GCCGGACGGC	1560
C	CGCTCTCC	A CGCT	GCTCTG	GCAGGCGATT	GCGGGGGCAT	GGCCGGCCAG	CCGGGAACGC	1620
C:	TCAGTCC	T ACGC	CCTGAA	AGCGGCGCGC	GAAGCCGGGA	ACTCGACCAG	CTGGACCGAT	1680
C	CGGACCCG	G CATT	CGAGGA	GGCACTTTCC	GCCGTCGTCG	ACTCCGCCTT	CGACAATCCG	1740
G	AGGTGCGT	g cgga	ACTTGA	GCCCTGGTG	GCCTCCTTG	CGCCGCACGG	TGCGTCCAAC	1800
T	CCTCCC	G CAAA	GCTTGT	CCAGCTGACC	ATGCCGGGCG	TTCCGGACGT	GTACCAGGGC	1860
A	CCGAGTTC	T. GGGA	CAGGTC:	GCTGACCGAT	CCGGACAACC	GGCGCCCCTT	CAGCTTCGCC	1920
G?	AACGGATT	A' GGGC	CTTGGA	CCAGTTGGAC	GCCGGCCACC	GTCCGGACTC	CTTCCAGGAC	1980
G?	AGGCGGTC	A AGCT	GCTGGT	CACCTCGAGG	GCGCTGCGGC	TGCGGCGGAA	CCGGCCCGAG	2040
C?	ICTTCACC	g gcta	CCGCCC	CGTGCATGCC	AGGGCCCCG	CCGCCGGGCA	CCTGGTGGCG	2100
T?	rcgaccgc	G GCGC	CGGGGG	AGTGCTGGCG	CTTGCCACCC	GGCTCCCCTA	CGGGCTGGAA	2160
C	AGTCGGGC	G GCTG	GCGGGA	CACCGCCGTC	GAGCTTGAAG	CCGCCATGAC	GGACGAACTG	2220
AC	CCGCTCC	A CTTT	CGGGCC	GGGACCGGCG	GCGCTGTCAG	AAGTCTTCCG	GGCCTACCCG	2280
G	rggccttg	T TGGT	CCCCGC	GACAGGAGG	C AAGTCA			2316

SEQ ID NO:3

5	GTGAACACGC	TCGCCGGCGT	CCGCGTGGAA	ATCCCCGCCG	TCTTCGACG	A GGCACACCA	G 660
	GAGGTGGTGC	GCTGGTTCCG	CGAGGACCTT	GCGGACGGCC	TGCGGATCG	A CCACCGGA	C 720
	GGCCTCGCTG	ACCCCGAGGG	GTACCTGAAG	CGACTCCGG	AAGTCACCG	G CGGCGCTTA	C 780
10	CTGCTGATCG	AAAAGATCCT	GGAGCCGGGG	GAGCAGCTGC	CCGCCAGCT	CGAGTGTGA	A 840
	GGCACCACAG	GCTACGACGC	CCTCGCCGAC	GTCGACCGGG	TTCTCGTGG	CCCGCGCGG	900
	CAGGAACCGC	TGGACCGGCT	TGACGCGTCC	CTGCGTGGCG	GCGAGCCCGG	CGACTACCA	G 960
15	GACATGATCC	GCGGAACCAA	GCGCCGGATC	ACCGACGGTA	TCCTGCACTC	GGAGATCCTG	1020
	CGGCTGGCCC	GGCTGGTTCC	GGGCGACGCC	AACGTTTCAA	TCGACGCCGG	AGCCGACGCT	1080
	CTCGCCGAAA	TCATCGCCGC	CTTCCCGGTC	TACCGCACCT	ACCTGCCGGA	GGGCGCGAG	3 1140
20	GTCCTGAAGG	AGGCGTGCGA	GCTTGCCGCG	CGTAGGCGGC	CGGAACTCGA	CCAGGCCATC	1200
	CAGGCTCTGC	AGCCGCTGCT	GCTGGACACG	GACCTCGAGC	TTGCCCGGCG	CTTCCAGCAG	1260
	ACCTCGGGCA	TGGTCATGGC	CAAGGGCGTG	GAGGACACCG	CGTTCTTCCG	CTACAACCGC	1320
25	CTGGGCACCC	TCACGGAAGT	GGGCGCCGAC	CCCACCGAGT	TCGCCGTGGA	GCCGGACGAG	1380
	TTCCACGCCC	GGCTGGCACG	CCGGCAGGCC	GAGCTTCCGC	TGTCCATGAC	GACGCTGAGC	1440
_	ACGCACGACA	CCAAGCGCAG	CGAGGACACC	CGAGCAAGGA	TTTCGGTCAT	TTCCGAGGTT	1500
30	GCGGGTGACT	GGGAAAAGGC	CTTGAACCGG	CTGCGCGACC	TGGCCCCGCT	GCCGGACGGC	1560
	CCGCTGTCCG	CGCTGCTCTG	GCAGGCCATT	GCCGGCGCCT	GGCCCGCCAG	CCGGGAACGC	1620
25	CTGCAGTACT	ACGCGCTGAA	GGCCGCGCGT	GAAGCGGGGA	ACTCGACCAA	CTGGACCGAT	1680
35	cceccccc	CGTTCGAGGA	GAAGCTGAAG	GCCGCGGTCG	ACGCCGTGTT	CGACAATCCC	1740
	GCCGTGCAGG	CCGAGGTGGA	AGCCCTCGTC	GAGCTCCTGG	AGCCGTACGG	AGCTTCGAAC	1800
40	TCCCTCGCCG	CCAAGCTCGT	GCAGCTGACC	ATGCCCGGCG	TCCCGGACGT	CTACCAGGGC	1860
40	ACGGAGTTCT	GGGACCGGTC	GCTGACGGAC	CCGGACAACC	GGCGGCCGTT	CAGCTTCGAC	1920
	GACCGCCGCG	CCGCGCTGGA	GCAGCTGGAT	GCCGGCGACC	TTCCCGCGTC	ATTTACCGAT	1980
45	GAGCGGACGA	AGCTGCTAGT	GACGTCGCGC	GCGCTGCGGC	TGCGCCGGGA	CCGTCCGGAG	2040
	CTGTTCACGG	GGTACCGGCC	GGTCCTGGCC .	AGCGGGCCCG	CCGCCGGGCA	CCTGCTCGCG	2100
	TTCGACCGCG	GCACCGCGGC	GGCGCCGGGT	GCATTGACCC	TCGCCACGCG	GCTTCCCTAC	2160
50	GGGCTGGAAC	AGTCGGGTGG	ATGGCGGGAC	ACCGCCGTCG	ÄACTTAÄCAC	CGCCATGAAA	2220
	GACGAACTGA (	CCGGTGCCGG	CTTCGGACCG	GGGGCAGTGA	AGATCGCCGA	CATCTTCCGG	2280
	TCGTTCCCCG	TTGCGCTGCT	GGTGCCGCAG	ACAGGAGGAG	AGTCA	••	2325

12. The replicable recombinant DNA as claimed in claim 11, wherein one or more bases in SEQ ID NOs:1 and 3 are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences of the following SEQ ID NOs:2 and 4 in this order:

SEQ ID NO:2 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg-Ile Arg Ile-Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu

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	Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Gli
	205		, ta			210					215					220	
10	Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
		· · · ;	<b>.</b> , .	225	•				230					235	: 2		
	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
15	•••	240					245					250	• .	•	ż	•	255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Glr
•	• ,	: ~		• ~	260					265					270	-	
20	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
	. 1 -	-:	275	•		~	-	280					285	•			
	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
25	290	. :	:	-		295					300					305	
	Leu	Asp	Ala	Arg	Leu	Arg	Ģly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	Asp	Met	Ile
30	•	• •		_310			٠,		315					320			
30	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu.	Ile	Leu
		325					330					335		٠	٠	<u>.</u>	340
35	Arg	Leu	Ala	Arg	Leu	Val	Pro	_Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glú	Ala	Ala
				. "	345					350					355		
	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
40			360					365					370				
	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	Ala	Cys	Asp	Leu	Ala	Ala	Arg
	375					380			•		385					390	
45	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
			•	395					400				:	405			
€.	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
50		410					415					420		*			425
	Met	Ala	ŗàs	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
		٠			430					435					440		

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5	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
			445					450					455				
	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
10	460		· •	• .		465					470					475	
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480	•				485					490			
15	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg
		495					500					505					510
	Leu	Asn.	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp
20					515			:		520					525	**	
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu.	Gln	Ser	Туг
	٠٠.		530					535					540		:		
25	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545			٠.		550	. ;				555			-		560	-
	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
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	Asn	Pro	Gľu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
		-580					585					590					595
35	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
					600					605					610		
40 "	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
40 "			615					620				•	625				•
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
45	630			•		635					640				4 - ·	645	₹
79	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Glu	Ala	Val
				650					655					660			
50	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
- <del>-</del>		665		•		:	670				. •	675	••				680
	Leu	Phe	Thr	Gly	туr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His

					685					690	I				695		
5	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
			700	1				705					710				
	Leu	Pro	Туг	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu
10	715					720					725					730	
	Leu	_G1u	Ala	Ala	Met	Thr	yab	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly
				735				·.	740				٠.	745			
15	Pro			Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Val
		750			. :		755				•	760			•		765
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	Leu	Phe	Asp	λla	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly		: -: ( Asp
35			20	-··		<del>-</del> - · -		25			** ,		30				
	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gly
	35					40	•		•		45					50	
ю	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55					60		٠.			<b>65</b> ,			
	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Leu
15		70					75	•				80					85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
50	٠			•	90					95					100		
-	Trp	Trp		Ser	Leu	Leu	Lys	Glu	Gly.	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
	_		105		•	•		110			٠.		115				
5		Asp	Val	Asp	Trp		Leu	Ala	Gly	Gly		Ile	Arg	Leu	Pro	Val	Leu
	120					125					130			· · ·		135	

5	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
				140				_	145					150			
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
10		155					160					165					170
	Ala	Pro	Arg	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
				•	175					180			`.		185		
15	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
			190					195					200				
	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
20	205					210					215					220	
	Val	Val	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
•				225					230					235			
25	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240				•	245					250					255
	Thr	Gly	Gĺy	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
30		•	=	•	260					265			•		270		
	Leu	Pro	Ala	Ser	Phe	Glu	Суз	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275		•			280	,				285				
35	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	290					295					300					305	
40	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
40				310				•	315					320		•	
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
45		325					330				•	335					340
45	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
					345					350					355		
50	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Ārg	Thr	Tyr
			360					365				•	370				
	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg

5	375	•				380					385					390	
		Arα	Pro	Glu	Leu	asA	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
				395		-			400			• .		405			
10		mb-	N a m		Gl II	Len	λla	Arg		Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
	Asp	1.	ASD	rea	Gra	Deu	415	7,29	y		<b></b>	420					425
		410	_	-1		<b></b>		mh		Dho	Pho		Mara-	A en	Ara	T.au	
15	Met	Ala	Lys	GTĀ		GIU	ASP	Thr	ATG		FILE	ALG	TYL	NSII	440		
					430		_	_	_	435	~1	<b>-</b> 1		**-1		D	3.00
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	GIU	Pne		va1	GIU	PIO	ASP
20			445					450					455		-	*	
20	Glu 	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu		.Met
	460			•		465	• •			•	470					475	
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
25	•		•	480		•	٠		485					490	•		
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
		495	-				500		; ,			505					510
30	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
					515					520					525	.·· .	
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
<b>35</b>			530		٠.	÷		535					540				
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
	545		_			550				•	555					560	
40			Ala	Phe	Glu		Lvs	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
				565					- 570					575			
	3	Dro	212			בוג	Glu	Val		Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
45	ASII		YTG	Val	GIII	7.4		• • • •	014			590	•		-		595
		580			_	_	585	• • •		<b>7</b>	T		Cln	Leu	ምb ም	Mot	*.* .*
	Tyr	Gly	Ala	Ser	*		Leu	Ala	АТа		Leu	Val	GIII	. Dea	• •	ne c	110
50				•	600					605	*	_			610	_	
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp			ser	Leu	Thr
			615					620					625				

5	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	Asp	Arg	Arg	Ala	Ala	Leu
•	630		. •			635					640					645	
	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr
o				650					655					660			
_	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu
		665					670					675					680
5	Leu	Phe	Thr	Gly	Týr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His
		. •			685					690					695		
	Leu	Leu	Ala	Phe.	qeA	Arg	Gly	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Ĺeu	Thr	Leu
0			700					705					710			sage was	
	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr
	715		•			720					725					730	·
25	Ala	Val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe
				735			. ;		740					745			:
	Gly	Pro	GĴY	Ala	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala
00		750	,				755					760					76.5
	Leu	Leu	Val	Pro	Gln	Thr	Gly	Gly	Glu	Ser							
				:	770					775		. ·. ·				·	- + -
			1														

13. The replicable recombinant DNA as claimed in claim 8, which has a base sequence selected from the group consisting of those as shown in SEQ ID NO:10 and 11:

#### SEQ ID NO:10:

35

50

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60
CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGC GGTGCCGATT CCGAACCCGT 120
GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180
CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240
TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300
GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360
GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGC 420

5	GAAG	GCCG	GAA G	AGAA	GGC	rc cc	GACG	AGGC	GGC	GGCG	AAG C	CCGGZ	AAGAG	G CI	GCTT(	CCGA	480
	CGA	GCG	GCG G	CGA	GCC	cg cg	GGGA	AGGC	AGC	GGCC	AAA A	ACGGG	CCGGC	CA GG	CGAG	CGCC	540
	AGG	CAAGO	CAG (	GCG	GGAC	GG G	CTC										564
10	ATG	AGG	ACA	CCC	GCC	TCG	ACC	TAC	CGG	CTG C	CAG A	ATC A	GG C	GG G	GT TI	rc	612
	Met	Arg	Thr	Pro	Ala	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Arg	Gly	Phe	
	1				5					10					15		
15	ACG	CTG	TTT	GAT	GCC	GCC	GAG	ACC	GTG (	CCC 1	TAC C	CTG A	AG I	CA C	TC GC	GG	660
	Thr	Leu	Phe	Asp	Ala	Ala	Glu	Thr	Val	Pro	Tyr	Leu	Lys	Ser	Leu	Gly	
				20					25					30		+4	
20	GTG	GAC	TGG	ATC	TAC	CTG	TCG	CCC	ATC (	CTG A	AAG (	GCA C	SAG A	GC G	GC TC	Ec	708
	Val	Asp	Trp	Ile	Tyr	Leu	Ser	Pro	Ile	Leu	Lys	Ala	Glu	Ser	Gly	Ser	
			35					40					45				
25	GAC	CAC	GGC	TAT	GAC	GTC	ACC	GAT	CCC	GCC 0	STA (	GTG G	AC C	CG G	AG CO	GC	756
	Asp	His	Gly	Tyr	Asp	Val	Thr	Asp	Pro	Ala	Val	Val	Asp	Pro	Glu	Arg	
		50					55					60					
30	GGC	GGC	CCT	GAA	GGG	CTG	GCC	GCG	GTG	TCC A	AAG (	GCG G	SCC C	GC G	GT GC	CC	804
	Gly	Gly	Pro	Glu	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	_Gly	Ala	
25	65					70			-		75					80	•
35	GGC	ATG	GGC	GTG	CTG	ATC	GAC	ATC	GTG	CCGT	AAC C	CAC G	STG G	GC G	TG GC	CG	852
	Gly	Met	Gly	Val	Leu	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	
40	-				85					90				•	95		
	TCG	CCG	CCG	CAG	AAC	CCG	TGG -	TGG	TGG	TCG (	CTG (	CTC A	LAG G	AA G	GG CC	3C	900
	Ser	Pro	Pro	Gln	Asn	Pro	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	
45				100					105					110			
	GGG	TCG	ccc	TAC	GCC	GTG	GCG <sub>.</sub>	TTC	GAC	GTC (	SAC 1	rgg (	AC C	CTG G	CG GC	GG .	948
	Gly	Ser	Pro	Tyr	Ala	Val	Ala	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	
50			115				,	120			. ,		125				
	GGC	CGC	ATC	CGG	ATC	CCC	GTC	CTG	GGC .	AGC G	AC C	GAC C	AT C	TG G	AC C	<b>A</b> G	996
	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	

5																	
J		130					135					140					
	CTC	GAA	ATC	AAG	GAC	GGC	GAG	CTG	CGG	TAC	TAC (	GAC C	CAC	CGC '	rTC (	CCG	1044
	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg	Тут	Tyr	Asp	His	Arg	g Pho	e Pro	
10	145					150					155					160	
	CTG	GCC	GAG	GGC	AGC	TAC	CGG	GAC	GGC	GAC	TCC C	CCG C	AG C	GAC (	GTC (	CAC	1092
	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp	Ser	Pro	Gln	Ası	va.	l His	
15					165					170					17	5	
	GGC	CGG	CAG	CAC	TAC	GAA	CTC	ATC	GGC	TGG	CGG (	GC G	CC G	SAC A	AAT (	GAA	1140
	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Ası	) Ası	n Glu	',
20				180					185	;				190	)	12.31	:
	CTG	AAC	TAC	CGC	CGG	TTC	TTC	GCG	GTG	AAC	ACG (	CTC G	CC G	GC 2	ATC (	CGG	1188
	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gl	, Ile	e Arg	
25			195					200	)				205	i	•		
	GTG	GAG	GTG	CCG	CCG	GTC	TTC	GAT	GAA	GCG	CAC C	CAG G	AG G	STG (	STG (	CGC	1236
	Val	Glu	Val	Pro	Pro	Val	Phe	· Asp	Glu	Ala	His	Gln	Glu	. Val	. Va	l Arg	
30		210	•	•			215					220					
	TGG	TTC	CGŤ	GCG	GGG	CTC	GCC	GAC	GGG	CTG	CGG 2	ATC G	ac c	CAC	CCG (	GAC	1284
	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His	Pro	o Asp	• •
35	225				-	230					235	•				240	
	GGC	CTG	GCC	GAT	ccc	GAG	GGG	TAT	TTG	AAG	CGG C	CTC C	GT G	AG (	STC A	ACC	1332
	4															l Thr	
10					245		<b>-</b>			250	•		J		25		
	GGG	GGC	GCG	TAC		CTC	ATC	GAA	AAG		CTC (	GAG C	cc c	GC (	GAA (	CAG	1380
																ı Gln	
15	OL,	CLY	n.c	260	Leu	LCu	110	014	265		. 204	0		270			
	mmc	ccc	CCC		mmc	CAC	mcc	CNA			ACC G	u	יאר כ			<b>-т-</b> -	1428
50	Leu	Pro			Pne	GIU	САЗ		_	THE	Thr				) VI	a Leu	
		· .	275					280					285		200	200	1.400
	GCG	GAT	GTC	GAC	AGG	GTC	TTC	GTG	GAC	CCG	CGG G	iGA C	AG G	FIG (	) قاتان	-TG	1476

5	Ala	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	
		290					295					300			,	bq ,	
	GAC	CGT	CTG	GAC	GCA	CGG	CTG	CGC	GGC (	GGT (	SCG (	CCG G	CC G	AC T.	AC G	AG	1524
10	Asp	Arg	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	
	305					310		•			315		:	_		320	
	GAC	ATG	ATC	CGC	GGG	ACC	AAG	CGC	CGG 2	ATC A	ACC (	GAC G	GC A	TC C	TG C	AC	1572
15	Asp	Met	Ile	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	·Ile	Leu	His	
					325					330	٠,				335		
	TCC	GAG	ATC	CTG	CGC	CTT	GCC	AGG (	CTG (	STG (	cc	GAG C	AG A	CC G	GA A	CT.	1620
20	Ser	Glu	Ile	Leu	.Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly.	Ile	**
				340					345	•		0. •	:	350	. 23	. 4	
	·ccc	GGG	GAG	GCG	GCC	GCG	GAT	GCG .	ATC (	SCG (	GAG A	ATC A	TC G	CG G	CC TI	rC	1668
25	Pro	Gly	Glu	Ala	Ala	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	
			355				ļ	360					365				,
30	CCG	GTC	TAC	CGG	TCC	TAT	CTT	ccc (	GAG (	GC (	GCG (	GAG A	TC C	TG A	AG GA	AG	1716
30	Pro	Val	Tyr	Arg	Ser	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	• .
		370					375				٠	380			:	ð-1	
35	GCC	TGC	GAC	CTC	GCC	GCG	CGG	AGG (	CGT (	CCG (	SAA C	CTG G	GC .C	AG A	CC G1	C.	1764
· ·	Ala	Cys	Asp	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	
	385					390					395					400	
40	CAG	CTG	CTG	CAG	CCG	CTG	CTG	CTG (	GAT A	ACC (	SAC C	CTC G	AG A	TT TO	cc co	€C	1812
	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	
					405		-			410				, .	415		
45	AGG	TTC	CAG	CAG	ACC	TCG	GGA	ATG (	GTC A	ATG C	GCC A	AA G	GC <sub>.</sub> G	TG G	AG GA	AC.	1860
	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	.,
-				420					425					430			
50	ACC	GCG	TTC	TTC	CGC	TAC .	AAC (	CGG (	CTG C	GA A	CG C	CTC A	CC G	AG G	rg gg	C	1908
	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
			435					440					445				

5	GCC	GAC	ccc	ACC	GAG	TTC	TCG	CTG	GAA (	CCG G	SAG C	GAG T	тт с	AC G	TC C	GG	1956
	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu	Glu	Phe	His	Val	Arg	
		450					455		-			460	•		٠.	****	-
10	ATG	GCC	CGC	CGG	CAG	GCC	GAA	CTC	CCG, (	CTC I	CC P	ATG A	CC A	cc c	TG A	GC	2004
	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	
	465					470				•	475					480	• .
15	ACG	CAC	GAC	ACC	AAG	CGC	AGC	GAG	GAC A	ACC C	GG C	CC C	GG A	TC T	CG G	rg	2052
	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
					485					490				:	495	18.95 18.95	(00)
20	ATC	GCC	GAG	GTC	GCG	CCT	GAA	TGG	GAA A	AAG C	CC C	CTG G	AC A	GG C	TG A	AC;®	2100
	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	ГЛЗ	Ala	Leu	Asp	Arg	Leu	Asn	-
	.: *			500					505			· ·		510	4.5.	D TE	כנת
25	ACC	CTC	GCT	CCG	CTG	CCG	GAC	GGC	CCG (	CTC 1	rcc #	ACG C	TG C	тс т	GG C	AG C	2148
	Thr	Leu	Ala	Pro	Leu	Pro	Asp	, Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp	Gln	
•	•		5 <b>1</b> 5					520		:	-		525		••		
30	GCG	ATT	GCG	GGG	GCA	TGG	CCG	GCC	AGC (	CGG .C	SÄA C	cec c	TT C	AG T	CC T	AC	2196
	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr	,
		530	. , <u>:</u> .		· ·.		535			:		540	-		() -		
35	GCC	CTG	AAA	GCG	GCG	CGC	GAA	GCC	GGG 2	AAC 1	rcg /	ACC A	GC T	GG A	CC G	AТ	2244
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	
	545					550		٠			555	•			٠.	560	
40	CCG	GAC	CCG	GCA	TTC	GAG	GAG	GCA	CTT '	rcc c	SCC (	GTC G	TC G	AC T	CC G	CC ·	2292
	Pro	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	
					565					570					575	• :	1
<b>45</b>	TTC	GAC	ААТ	CCG	GAG	GTG	CGT	GCG	GAA (	CTT (	GAG (	GCC C	TG G	TG G	GC C	TC ?	2340
	Phe	Asp	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	
	••	,		580					585					590	٠.	•	
50	СТТ	GCG	CCG	CAC	GGT	GCG	TCC	AAC	TCG (	CTC (	GCG (	GCA 7	AG C	TT G	TC C	AG	2388
	Leu	Ala	Pro	His	Gly	Ala	Ser	Asr	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	

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d2

5			595					.600	t				605	5	•		
	CTG	ACC	ATG	CCG	GGC	GTT	CCG	GAC	GTG	TAC	CAG	GGC F	ACC (	GAG	TTC 1	rgg	2436
	Leu	Thr	Met	Pro	Gly	val	Pro	) Asp	Val	Tyr	Glr	ı Gly	Thr	Gl	u Phe	Trp	,
10		610					615	;				620				-	
	GAC	AGG	TCG	CTG	ACC	GAT	CCG	GAC	AAC	CGG	CGC	CCC 1	TTC	AGC	TTC C	CC	2484
	Asp	Arg	Ser	Leu	Thr	Asp	Pro	) Asp	Asn	Arg	Arg	, Pro	Phe	Sez	. Phe	. Ala	
15	625					630	)				635	5				640	
	GAA	CGG	ATT	AGG	GCC	TTG	GAC	CAĢ	TTG (	GAC (	GCC (	GGC C	AC (	CGT (	CCG G	FAC	2532
	Glu	Arg	Ile	Arg	Ala	Leu	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	J Pro	Asp	
20					645					650					655	i .	
	TCC	TTC	CAG	GAC	GAG	GCG	GTC	AAG	CTG (	CTG (	GTC .	ACC T	'CG A	AGG (	GCG C	ŢG	2580
25	Ser	Phe	Gln	Asp	Glu	Ala	Val	Lys	Leu	Leu	Val	Thr	Ser	Arc	, Ala	Leu	
23				660					665					670			
	CGG	CTG	CGG	CGG	AAC	CGG	CCC	GAG (	CTC :	TTC A	ACC (	GGC T	AC C	CGC (	CCC G	TG	2628
30	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	
			675					680					685		÷		٠.
	CAT	GCC	AGG	GGC	CCC	GCC	GCC	GGG (	CAC	CTG (	STG (	GCG T	TC G	AC C	CGC G	GC	2676
35	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His	Leu	Val	Ala	Phe	Asp	Arg	Gly	
		690					695					700			,		
	GCC	GGG	GGA	GTG	CTG	GCG	CTT (	GCC A	ACC C	GG C	CTC C	CCC T	AC G	igg c	TG G	AA	2724
40 ·	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	
	705					710	•				715					720	
												CTT G					2772
45	-Gln	Ser	Gly	Gly	Trp	Arg	ysb	Thr	Ala	Val	Glu	Leu	Glu	Ala	Ala	Met	
					725					730					735		
												GA C					2820
50	Thr I	qeA	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly	Pro	Ala	Ala	Leu	
				740					745					750			
	TCA (	SAA (	GTC 1	rtc (	CGG (	GCC 1	rac c	CCG G	TG G	CC T	TG T	TG G	rc c	CC G	CG Ä	CA	2868

i.

100

	*																	
5	Ser	Glu	Val 755	Phe	Arg	Ala	Tyr	Pro 760	Val	Ala	Leu	Leu	Val 765	Pro	Ala	Thr		
3	GGA	GGC	AAG	TCA									/03					-
		Gly															2880	
	_	770	-1	-	-					-,						The ATT		
10										,							•	
	TGAC	GCAC	CC C	AACG	ATGC	G GC	CAAG	CCGG	TGC	\GGGA	GC G	GGGC	GCTT	C GA	TATC	2	936	
								•	•		•							
15					·			•										
							•											
						- 1	•••											
20													. •		;	e constant	<u> </u>	
												1						
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25	,			*	: :			•		· ·			. •		C .3.1	T te		_; <del>"</del>
							į							<b>3</b> %		7 3.3	:	
<b>30</b>		,	• • ••	. • ••									. •					
				· a	•													
35														<u>-</u> ,	<b>-</b> .*	and the same of th		

5	SEQ ID NO:11				
	GATCCGGACG GCAACG	TCAT GTCCCCGGAG GACT	GGACA GCGGCTTCGG	CCGTTCGGTG	60
10	GGCATGTTCC TCAACO	GCGA CGGCATCCAG GGCC	CGATG ACCGCGGCCG	CCGCATCACG	120
	GACGTGAACT TCCTG	TGTA CTTCAACGCC CACGA	CGGCG ACGTCGAGTT	CACGCTGCCG	180
	CCGGACGAAT ACGCCC	CGGC CTGGGACGTC ATCAT	CGACA CCGCCGGTGA	AGGGGCCGAC	240
15	TCCAAGCCCG CGGACG	CCGG AACCATCCTG TCCGT	TGCGG CCAAGTCGCT	GGTTGTGCTT	300
	CGCGCCCACA GCGCAC	CGGA GGAGGAGCCT GACCA	TTCCG TGGCTGCTTC	CCTGGCTGCA	360
	CTGACGCAGA CCGCCA	CCGC CGAGACGGCG GCGCT	CACAG CTCCTGCCGT	TCCCGAGCCG	420
20	GCCAAGACGA AGAAGC	CGGC CGCTGACCCG GTTGC	TGAAC CGGCCGACCC	GCCGGTTGCT	480
		TTGC TGACCCGGTT GCTGA			540
		CGGA ACCTGGTGCG GAGCC			
25		GCAA GCCTGCGGCA AAGCG	CGGCG GCCACCTGAG	GCGGTCAAG	660
	CCCGCTGGGG AGGACG				677
		TC TCC ACG TAC AGG CT			725
30	Met Arg Thr Pro V	al Ser Thr Tyr Arg L	eu Gln Ile Arg Ly	s Gly Phe	٠.
	1 5			15	
		CG GCC AAA ACC GTT CC	,		773
35	Thr Leu Phe Asp A	la Ala Lys Thr Val P	ro Tyr Leu His-Se	r Leu Gly	
	20	<b>25</b>	30	3	
		C CTT TCT CCG GTC CTC			321
<del>1</del> 0		yr Leu Ser Pro Val Le	eu Thr Ala Glu Gl	n Gly Ser	
	35	40	45		

5	GAC	CAC	GGG	TAC	GAC	GTC	ACC	GAT	CCC	TCC (	GCC (	STC G	AC C	CC G	AA C	GC	869
	Asp.	His	Gly	Tyr	Asp	Val	Thr	qe,	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	
		50					55					60					
10	GGC	GGG	CCG	GAG	GGC	CTC	GCG	GČG	GTT	TCC 2	AAG (	GCG G	cc c	GC G	CC G	CG .	917
	Gly	Gly	Pro	Glu	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	
	65					70					75					80	
15	GGC	ATG	GGC	GTG	CTG	ATC	GAC	ATC	GTG (	ccc i	AAC C	CAC G	TG G	GC G	TC G	CG	965
	Gly	Met	Gly	Val	Leu	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	
					85					90			٠.		95		
20	ACG	CCG	GCG	CAG	AAC	ccc	TGG	TGG	TGG '	TCG (	CTG C	CTC A	AG G	AG G	GA C	GC	1013
	Thr	Pro	Ala	Gln	Asn	Pro	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	
	•			100					105					110		•.*	
25	CAG	TCC	CGT	TAC	GCG	GAG	GCG	TTC	GAC	GTC (	GAT I	rgg g	AC C	TC G	CC G	GG	1061
	Gln	Ser	Arg	Tyr	Ala	Glu	Ala	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	
			115		•			120	r				125				
30	GGA	CGC	ATC	CGG	CTG	CCG	GTG	CTC	GGC 2	AGC (	GAC G	SAT G	AC C	TC G	AC C	AG	1109
	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	
35	1.	130		5143	· · ·	-	135					140					
35	CTC	GAA	ATC	AGG	GAC	GGG	GAG	CTG	CGG	TAC !	rac c	GAC C	AC C	GA T	TC C	CG	1157
	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	Arg	Phe	Pro	
40	145	,				150				•	155					160	
••	CTC	GCC	GAG	GGA	ACC	TAC	GCC.	GAA	GGC (	GAC (	GCC C	CCG C	GG G	AT G'	TC C	AC	1205
-	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp	Ala	Pro	Arg	Asp	Val	His	
45					165			-		170					175	-1	
	GCC	CGG	CAG	CAC	TAC	GAG	CTC	ATC	GGC '	TGG (	CGC C	CGC G	CG G	AC A	AC G	AG	1253
	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Asp	Asn	Glu	
50			•	180					185					190			
											ACG C						1301
4	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gly	Val	Arg	

5			195					200					20	5			
	GTG	GAA	ATC	CCC	GCC	GTC	TTC	GAC	GAG (	GCA	CAC	CAG	GAG	GTG	GTG	CGC	1349
	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	s Glr	ı Gl	u Va	al Va	al A	rg
10		210					215					220	ס				
	TGG	TTC	CGC	GAG	GAC	CTT	GCG	GAC	GGC (	CTG	CGG	ATC	GAC	CAC	CCG	GAC	1397
	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	j Ile	e As	р Н	ls P	co As	sp ·
15	225					230					235	5				24	10
	GGC	CTC	GCT	GAC	CCC	GAG	GGG	TAC	CTG Z	AAG	CGA	CTC	CGG	GAA	GTC	ACC	<sub>6</sub> 1445
	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	g Le	ı Ar	g G	Lu V	al Tì	r <sub>j40</sub>
20					245					250					2	55. 🔭	. alo
	GGC	GGC	GCT	TAC	CTG	CTG	ATC	GAA	AAG A	ATC	CTG	GAG	CCG	GGG	GAG	CAG	1493
	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Le	ı Glı	ı Pr	o GI	Ly G	lu G	ln
25				260					265					27	70		
	CTG	CCC	GCC	AGC	TTC	GAG	TĢT	GAA	GGC .	ACC	ACA	GGC	TAC	GAC	GCC	CTC	1541
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Th	r Gly	у Ту	r As	A qu	la Le	eu <sub>.</sub>
30			275			. •		280	١.	·			28	15			
	GCC	GAC	GTC	GAC	CGG	GTT	CTC	GTG	GAC (	CCG	CGC	GGC	CAG	GAA	CCG	CTG	1589
35	Ala	Asp	Val	Asp	Arg	Val	Ļeu	Val	Asp	Pro	Arg	g Gly	y Gl	n G	Lu P	ro Le	au <sub>, De</sub> g
33		290					295					300	0		-	· ., : •	:i . 7.
	GAC	CGG	CTT	GAC	GCG	TCC	CTG:	CGT	GGC (	GGC	GAG	CCC	GCC	GAC	TAC	CAG	1637
40	Asp	Arg	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Gl	u, Pro	o Al	.a As	зр Т	yr G	ln .
	305					310	•				31	5				32	20
	GAC	ATG	ATC	CGC	GGA	ACC	AAG	CGC	CGG .	ATC	ACC .	GAC	GGT	ATC	CTG	CAC	1685
45	Asp	Met	Ile	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Th	r As	p G1	y 11	le L	eu H	İs
					325					330	)	. •		, .	3:	35 .	
	TCG	GAG	ATC	CTG	CGG	CTG	GCC	CGG	CTG (	GTT	CCG	GGC	GAC	GCC	AAC	GTT	1733
50	Ser	Glu	Ile	Leu	Arg	Leu	Ala	Arg	Leu	Val	. Pro	o Gly	y As	sp A.	la A	sn Va	al
				340					345					35	50 .		
	TCA	ATC	GAC	GCC	GGA	GCC	GAC	GCT	CTC (	GCC	GAA	ATC	ATC	GCC	GCC	TTÇ	1781

5	Ser	Ile	Asp	Ala	Gly	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	
			355					360		•		•	365		•	٠	
	CCG	GTC	TAC	CGC	ACC	TAC	CTG	CCG	GAG (	GC G	CC C	AG G	TC C	TG A	AG G	AG	1829
10	Pro	Val	Tyr	Arg	Thr	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	
		370					375					380					
	GCG	TGC	GAG	CTT	GCC	GCG	CGT	AGG	CGG (	CCG G	AA C	TC G	AC C	AG G	CC A	TC	1877
15	Ala	Cys	Glu	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	
	385					390				•	395					400	
•	CAG	GCT	CTG	CAG	CCG	CTG ·	CTG	CTG	GAC 2	ACG G	AC C	CTC, G	AG C	TT G	CC C	GG <sup>.</sup>	1925
20	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	
					405					410					415	, -	
	CGC	TTC	CAG	CAG	ACC	TCG	GGC	ATG (	GTC 1	ATG G	SCC A	AG G	GC G	TG G	AG G	AC ·	1973
25	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	
				420		·	٠;		425	· 		•		430		• •	
	ACC	GCG	TŤC	TTC	CGC	TAC	AAC	CGC	CTG (	GGC A	cc c	CTC A	.CG G	AA G'	TG G	GC	2021
30	Thr	Ala	Phe	Phe	Arg	Tyr	Àsn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
***			435					440		٠	••	٠	445				
	GCC	GAC	ccc	ACC	GAG	TTC	GCC	GTG (	GAG (	CCG G	AC C	AG T	TC C	AC G	cc c	GG	2069
35	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp	Glu	Phe	His	Ala	Arg	
		450					455	•				460					•
	CTG	GCA	CGC	CGG	CAG	GCC	GAG	CTT (	CCG (	CTG I	CC A	TG A	CG A	CG C	rg A	GC	2117
40	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	
	465					470					475		•			480	
	ACG	CAC	GAC	ACC	AAG	CGC	AGC	GAG (	GAC 2	ACC C	GA G	са а	GG A	TT T	CG G	TC	2165
45	Thr	Ήis	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
					485					490					495	•	
50	ATT	TCC	GAG	GTT	GCG	GGT	GAC	TGG (	GAA A	AAG G	cc 1	TG A	AC C	GG C	rg C	GC	2213
<i></i>	Ile	Ser	Ğlu	Val	λla	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg	Leu	Arg	
				500					505					510			

..(.<del>)</del>(.).

5	GAC	CTG	GCC	CCG	CTG	CCG	GAC	GGC	CCG	CTG	TCC	GCG	CTG (	CTC	TGG	CAG	2261
	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	. Leu	Le	u Tr	p Gln	
	•		515					520					525	i			
10	GCC	ATT	GCC	GGC	GCC	TGG	ccc	GCC	AGC (	CGG	GAA	CGC	CTG C	CAG	TAC	TAC	2309
	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	, Leu	Gl	п Ту	r Tyr	
	٠.	530	•		•		535					540	)				-
15	GCG	CTG	AAG	GCC	GCG	CGT	GAA	GCG	GGG .	AAC	TCG .	ACC .	AAC 1	rgg	ACC	GAT	2357
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thi	Asn	Tr	p Th	r Asp	
	545					550					555	i	- 4			560	
20	CCG.	GCC	CCC	GCG	TTC	GAG	GAG	AAG	CTG	AAG	ĢCC	GCG	GTC (	GAC	GCC	GTG	2405
	Pro	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	val	As	p Al	a Val	
		•			565	•				570	)			•	57	5	
25	TTC	GAC	AAT	ccc	GCC	GTG	CAG	GCC	GAG	GTG	GAA	GCC	CTC C	FTC	GAG	CTC	2453
	Phe	Asp.	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	. Glu	ı Ala	. Leu	۷a.	1 G1	u Leu	
				580			1,		585		:			59	0		
30	CTG	GAG	CCG	TAC	GGA	GCT	TCG	AAC	TCC	CTC	GCC	GCC .	AAG C	CTC	GTG	CAG	2501
	Leu	Glu	Pro	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	a Ala	Lys	Le	u Va	l Gln	
25			595				_	600	) 				605	0			
35	CTG	ACC	ATG	CCC	GGC	GTC	CCG	GAC	GTC	TAC	CAG	GGC	ACG C	SAG	TTC	TGG	2549
	Leu	Thr	Met	Pro	Gly	Val	Pro	Asp	Val	Туг	Glr	Gly	Thr	G1	u Ph	e Trp	
40		610					615					620	)	4.			•
₩	GAC	CGG	TCG	CTG	ACG	GAC	CCG	GAC	AAC	CGG	CGG	CCG	TTC A	AGC	TTC	GAC	2597
	Asp	Arg	Ser	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Se	r Ph	e Asp	
45	625					630		-			635	5				640	
.,,,,	GAC	CGC	CGC	GCC	GCG	CTG	GAG	CAG	CTG	GAT	GCC	GGC	GAC (	CTT	CCC	GCG	2645
•	Asp	Arg	Arg	Ala	Ala	Leu	Glu	Gln	Leu	Asp	Ala	Gl <sub>3</sub>	/ Asp	Le	u Pr	o Ala	
50					645	•				650	)				65	5	•
	TCA	TTT	ACC	GAT	GAG	CGG	ACG	AAG	CTG	CTA	GTG	ACG	TCG (	CGC	GCG	CTG	2693
	Ser	Phe	Thr	Asp	Glu	Arg	Thr	Lys	Leu	Leu	val	Thi	: Ser	Ar	g Al	a Leu	

5				660					665					670	)	•	
	CGG	CTG	CGC	CGG	GAC	CGT	CCG	GAG (	CTG 1	TC A	.CG G	GG T	AC C	GG (	CCG	GTC	2741
	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	, Pr	o Val	
10			675					680					685				
	CTG	GCC	AGC	GGG	ccc	GCC	GCC	GGG (	CAC (	CTG C	TC G	CG T	TC G	AC (	CGC	GGC	2789
	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His	Leu	Leu	Ala	Phe	Ası	) Ar	g Gly	
15		690					695					700					
	ACC	GCG	GCG	GCG	CCG	GGT	GCA	TTG 2	ACC (	CTC G	CC A	CG C	GG C	TT (	CCC	TAC	2837
	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu	Ala	Thr	Arg	Let	Pr	о Туг	:
20	705			•		710					715					720	C .
	GGG	CTG	GAA	CAG	TCG	GGT	GGA	TGG (	CGG (	GAC A	CC G	CC G	TC G	AA (	CTT	AAC	2885
	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Gli	ı Le	u Asn	ı
25			·		725					730					73	5	
	ACC	GCC	ATG	AAA	GAC	GAA	CTG	ACC (	GGT (	GCC G	GC I	TC G	GA C	CG (	GGG	GCA	2933
	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe	Gly	Pro	Gl	y Ala	
30			•	740	÷	-			745					750	)		
	GTG	AAG	ATC	GCC	GAC	ATC	TTC	CGG	TCG 1	rtc (	CC G	STT G	CG C	TG (	CTG	GTG	2981
	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala	Lev	ı Le	u Val	
<b>35</b> .			755			٠.		760				•	765				
	CCG	CAG	ACA	GGA	GGA	GAG	TCA									٠	3002
	Pro	Gln	Thr	Gly	Gly	Glu	Ser			•							
40		770		, s			775	•									
	TGA	CGCA	CAC (	CTAC	CCGC	GG GA	AGCC	GCGA	AAC	CCGT	CCT G	GGCC	CCGC	A C	CTA	CGACC	3062
	TCT	GGC	GCC	С													3073
45																	

14. The replicable recombinant DNA as claimed in claim 8, wherein said DNA is derived from a microorganism selected from the group consisting of those of the genera Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium and Terrabacter.

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- 15. The recombinant DNA as claimed in claim 8, wherein said self-replicable vector is a plasmid vector Bluescript II SK(+).
- 16. A transformant obtainable by introducing into a suitable host a recombinant DNA containing the DNA of claim 1 and a self-replicable vector.

- 17. The transformant as claimed in claim 16, wherein said DNA encodes an enzyme having the following physicochemical properties:
  - (1) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PA-GE): and

(2) Isoelectric point (pl)

About 3.6-4.6 on isoelectrophoresis.

- 18. The transformant as claimed in claim 16, wherein said DNA encodes an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:
- 15 SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

1 5 10 15

20 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

25 35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

**30** 

35

40

43

												•					
5	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Gly	Ala	Gly	Met	Gly	Val	Leu
		70					75					80				·42.	85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Ser	Pro	Pro	Gln	Asn	Pro
10				• .*	90		,		٠.٠,	95					100		
	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gly	Ser	Pro	Tyr	Ala	Val	Ala
			105					110					115				
15	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu
	120					125					130					135	
	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg
20				140				•	145				1	150		51 4	
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp
	*	155					160					165					170
25	Ser	Pro	Gln	Asp	Val	His	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
					175		į			180		٠			185	٠.	
	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
30			190					195		•		٠.	200			•	
	Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
	205					210		-	<b>-</b> . ∋		215				* <del>-</del> ·	220	
35	Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225					230					235			
	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
40		240			•		245					250					255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
					260					265					270		
45	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275					280					285				
50	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
50	290					295					300					305	
	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	туг	Glu	Asp	Met	Ile

5	•			310					315				•	320	•	••	
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Lev
	·	325					330					335					340
10	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
		ŧ '.		٠	345	¥ +				350					355		
	Ala	Asp	^Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Туг
15			360	-				365				,	370	· .		•	_= 0
	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	Ala	Cys	Asp	Leu	Ala	Ala	Arg
	375	•	٠.	-			-	•			385				20	390	
20	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
			- 4	395	•				400				•	405			
	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
25		410					415					420		•	,		425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
		٠			430	• .	· c			435		٠.	er,		440		
30	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu.	Pro	Glu
		'	445					450					455	_	<u>-</u>	ភូទ .	÷
	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
35	460	•				46,5	. :			٠.	470					475	
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480		•			485					490			
40	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg
		495					500					505	٠				510
	Leu.	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp
45					515					520			•		525		
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr
			530	ř			-	535			J	*	540				
50	Ala	Leu		Ala	Ala	Arg	Glu		Glv	Asn	Ser	Thr		Trp	Thr	Asp	Pro
	545					550			•		555			•		560	
																-	

5	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
3				565	- 4				570					575		Age .	
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
10		580					585					590					595
	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
		,			600					605					610	•	
15	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	тгр	Asp	Arg	Ser	Leu	Thr
		:	615					620					625				
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
20	630					635					640					645	-
	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Glu	Ala	Val
				650					655			,		660			
25	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
		665	٠				670					675					680
	Leu	Phe-	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
<b>30</b>			·		685					690					695		
	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
			700			•		705			• .:		710			•	
35	Leu	Pro	Туг	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu
	715	•	, .			720					725					730	
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly
40				735					740					745			
	Pro	Ala	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Val
•		750					755					760					765
45	Pro	Ala	Thr	Gly	Gly	Lys	Ser							•			
•		• • •			770				·			-					

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SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

5	1				5					10					15		
		Pha	Acn	Ala		 Lvs	Thr	Val	Pro	Tvr	Leu	His	Ser	Leu	Gly	Val	Asp
	Leu	FILE		,,,,		_,_		25		-4-			30		•		_
10	_	:	20	Leu	 Cara	 D	17-7		mb ~	31-	C1	Cln.		Sar	lan	Hie	ឲាម
10	-	Val	Tyr	Leu	Ser		AGT	Leu	IIIL	WTG.		GIM	GIY	Jer	vaħ	50	<u></u>
	35				.: .	40					45	~1	•	<b>61</b>		•	
45	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala		Asp	Pro	GIu	Arg		GIĀ	Pro	GIU
15				55					60					65		<b>.</b> .	_
	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Leu
		70	. :				75					80					85
20	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
					90					95					100		
	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
25			105					110	·				115				
	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu
	120			•		125	i,				130					135	
30	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
	_			140			•		145					150		:	
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
35		155	·		÷ 1-		160	. ()	:			165					170
	Ala		Ara	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
	-;		5	•	175				÷	180				-	185	•	
40	Ara	λla	Asn	Asn		Leu	Asn	Tvr	Ara	Ara	Phe	Phe	Ala	Val	Asn	Thr	Leu
	ALG	VIG	190	AGII	010			195	5				200				
				Arg	wal	Clu	TIO		. או	Val	Pha	Acn		Ala	His	Gln	Glu
45		GIY	vai	Arg	Val		TTE	PIO	VIG				014			220	
	205	_				210			-		215		<b>T</b>	3	710		
	Val	Val	Arg	Trp	Phe	Arg	GLu	Asp		ATS	Asp	GLY	Leu		TTE	ASP	nrs
50				225					230					235			
	Pro	qsA	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	
		240			:		245					250					255

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5	Thr	Gly	Gly	Ala	ту:	Le	ı Leu	lle	Glu	Lys	: Ile	Leu	Glu	Pro	Gly	, Glu	Glr
					260	)				265	<b>i</b>	·			270	)	
	Leu	Pro	Ala	Ser	Phe	Glu	ı Cys	Glu	Gly	Thr	Thr	Gly	Туг	Asp	Ala	Leu	Ala
0			275					280	••			•	285				
	Asp	Val	Asp	Arg	y Val	Lev	val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	290	)				295	j				300	)	•			305	
5	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
			•	310	)				315					320	,		
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
20	•	325					330					335	•			•	340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
25	•.		•		345					350			•		355	•	• 🖪 •
	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Tyr
•	•		360			•		365	•			•	370				
30	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg
	375	-	•	•		380			•.	•	385					390	
	Arg	Arg	Pro	Glu	Leu	yab	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
35				395					400	` a		., . + • =		405		-	
	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410				÷	415					420		•			425
40	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
					430					435			·		440		
	Thr	Leu	Thr	Glu	Val	Gly.	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp
45			445					450		٠			455		-		
	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460					465			:	•	470					475	
50	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480					485			٠. ٢	٠	490			
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg

											•						
5		495					500		, .	٠,		505			•	.i	510
	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
					515				•	520				•	525		
10	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
•			530		,_			535	•		·		540				
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn.	Ser	Thr	Asn	Trp	Thr	Asp	Pro
15	545					550					555					560	
	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
20				565					570					575	•		
20	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
		580					585					590				• . '	595
25	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
			٠.		600			• . •		605				٠	610	: .	:
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
30			615	÷ ,		.• .		620			•		625				
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	Asp	Arg	Arg	Ala	Ala	Leu
	630					635					640					645	
35	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr
				650		:		*	655					660	-	٠.,	
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu
40		665	-				670					675					680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His
			:		685			•		690					695		
45	Leu	Leu	Ala	Phe	Asp	Arg	Gly	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu
			700					705					710		• .	. 1	. * *
	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr
 <b>50</b>	715	**				720					725	÷.				730	
	Ala	Val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe
				735		,			740					745			

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
770 775

19. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

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SEO ID NO:1.

ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180 GACCCGGAGC GCGCCGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240 GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCCGCAG 300 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480 CTGGCCGAGG GCAGCTACCG\_GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540 TACGAACTCA TCGGCTGGCG GCGCCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660 GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGCG GTGCGCCGGC CGACTACGAG 960 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080

5	ATCGCGGAGA	TCATCGCGGC	CTTCCCGGTC	TACCGGTCCT	ATCTTCCCGA	GGGCGCGGAG	1140
	ATCCTGAAGG	AGGCCTGCGA	CCTCGCCGCG	CGGAGGCGTC	CGGAACTGGG	CCAGACCGTC	1200
	CAGCTGCTGC	AGCCGCTGCT	GCTGGATACC	GACCTCGAGA	TTTCCCGCAG	GTTCCAGCAG	1260
10	ACCTCGGGAA	TGGTCATGGC	CAAAGGCGTG	GAGGACACCG	CGTTCTTCCG	CTACAACCGG	1320
	CTGGGAACGC	TCACCGAGGT	GGGCGCCGAC	CCCACCGAGT	TCTCGCTGGA	ACCGGAGGAG	1380
	TTTCACGTCC	GGATGGCCCG	CCGCCAGGCC	GAACTCCCGC	TCTCCATGAC	CACCCTGAGC	1440
15	ACGCACGACA	CCAAGCGCAG	CGAGGACACC	CGGCCCGGA	TCTCGGTGAT	CGCCGAGGTC	1500
	GCGCCTGAAT	GGGÄAAAGGC	CCTGGACAGG	CTGAACACCC	TCGCTCCGCT	GCCGGACGGC	1560
	CCGCTCTCCA	CGCTGCTCTG	GCAGGCGATT	GCGGGGGCAT	GGCCGGCCAG	CCGGGAACGC	1620
20	CTTCAGTCCT	ACGCCCTGAA	AGCGGCGCGC	GAAGCCGGGA	ACTCGACCAG	CTGGACCGAT	1680
	CCGGACCCGG	CATTCGAGGA	GGCACTTTCC	GCCGTCGTCG	ACTCCGCCTT	CGACAATCCG	1740
	GAGGTGCGTG	CGGAACTTGA	GCCCTGGTG	GCCTCCTTG	CGCCGCACGG	TGCGTCCAAC	1800
25	TCGCTCGCGG	CAAAGCTTGT	CCAGCTGACC	ATGCCGGGCG	TTCCGGACGT	GTACCAGGGC	1860
	ACCGAGTTCT	GGGACAGGTC	GCTGACCGAT	CCGGACAACC	GGCGCCCCTT	CAGCTTCGCC	1920
	GAACGGATTA	GGGCCTTGGA	CCAGTTGGAC	GCCGGCCACC	GTCCGGACTC	CTTCCAGGAC	1980
30	GAGGCGGTCA	AGCTGCTGGT	CACCTCGAGG	GCGCTGCGGC	TGCGGCGGAA	CCGGCCCGAG	2040
	CTCTTCACCG	GCTACCGCCC	CGTGCATGCC	AGGGCCCCG	CCGCCGGGCA	CCTGGTGGCG	2100
	TTCGACCGCG	GCGCCGGGG	AGTGCTGGCG	CTTGCCACCC	GGCTCCCCTA	CGGGCTGGAA	2160
35	CAGTCGGGCG	GCTGGCGGGA	CACCGCCGTC	GAGCTTGAAG	CCGCCATGAC	GGACGAACTG	2220
- *	ACCGGCTCCA	CTTTCGGGCC	GGGACCGGCG	GCGCTGTCAG	AAGTCTTCCG	GGCCTACCCG	2280
	GTGGCCTTGT	TGGTCECCGC	GACAGGAGGC	AAGTCA			2316

*;* . :

	SEQ ID NO:	3			·		
5	ATGAGAACGC	CAGTCTCCAC	GTACAGGCTG	CAGATCAGGA	AGGGATTCAC	ACTCTTCGAC	60
	GCGGCCAAAA	CCGTTCCGTA	CCTGCACTCG	CTCGGCGTCG	ACTGGGTCTA	CCTTTCTCCG	120
	GTCCTGACTG	CCGAGCAGGG	CTCCGACCAC	GGGTACGACG	TCACCGATCC	CTCCGCCGTC	180
10	GACCCCGAAC	GCGGCGGCC	GGAGGGCCTC	GCGGCGGTTT	CCAAGGCGGC	CCGCGCCGCG	240
	GGCATGGGCG	TGCTGATCGA	CATCGTGCCC	AACCACGTGG	GCGTCGCGAC	GCCGGCGCAG	300
	AACCCCTGGT	GGTGGTCGCT	GCTCAAGGAG	GGACGCCAGT	CCCGTTACGC	GGAGGCGTTC	360
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GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540 10 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720 15 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900 20 CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080 25 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140 GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260 30 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320. CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380 TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440 35 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620 40 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680 CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980 50 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040 CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100

TTCGACCGCG GCACCGCGCC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220
GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

20. The transformant as claimed in claim 19, wherein one or more bases in SEQ ID NOs:1 and 3 are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences as shown in the following SEQ ID NOs:2 and 4:

SEQ ID NO:2 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu .80 . . . . . . . . . . . . . Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp 

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5	Ser	Pro	Gln	Asp	Val	His	Gly	Arg	Gln	His.	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
					175		-			180			<u>_</u> ,.	.~	185		
	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
10	*	:	190			j.		195	- :		į -		200	٠.			
	Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
	205			;		210					215					220	
15	Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225					230					235			~ <u>7</u>
	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu.	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
20		240					245				,	250			, <u>.</u> .	- ] .	255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
				٠.	260					265					270		
25	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275				.j	280					285				
30	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
•	290					295				•	300			٠		305	
	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	Asp	Met	Ile
35				310	. ,				315				in the	320			
-0	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325					330					335					340
40	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
•					345		٠			350					355		
	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
45			360		,	÷ .		365					370				
	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	Ala	Cys	Asp	Leu	Ala	Ala	Arg
	375			:		380			٠,		385		· · · · · ·			390	
50	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
			•	395					400					405			
	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val

									•								
5		410					415					420					425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
					430					435		•			440		
10	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
		•	445					450					455				
15	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
,,	460					465			•		470					475	
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Аsp	Thr	Arg	Ala	Arg
20		·		480					485			٠		490			
	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg
		495					500			•		505		•			510
25	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr			
					515					520						#R 1.	
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr
30			530	•			•	535	•	•			540				
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545					550	•				555					560	
35	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
				565		•		,	570					575			
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	
40		580					585					590					595
	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
					600					605		•			610		
45	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
	•		615					620					625				
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
50	630			٠.,	-,- ,	635			٠		640					645	•
	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Glr	Asp	Glu	. Ala	Val
				650	I				655	i				660	)		

	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
5		665					670					675					680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
	·				685					690					695		
10	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
•			700					705					710				
	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu
15	715					720			•		725					730	
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly
				735					740		•			745			
20	Pro	Ala	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Val
		750					755					760					765
	Pro	Ala	Thr	Gly	Gly	Lys	Ser				•						
25					770												

		•															
								•					٠-				
5	SEQ	ID I	10:4														
	Met	Arg	Thr	Pro	Val	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Lys	Gly	Phe	Thr
	1				5					10					15		
40	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	Val	Asp
10	•		20					25					30	;	. :		
	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gly
	35				•	40				·	45		•			50	
15	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55					60	٠				65			
	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Leu
20		70					75		•		•	80				Is	85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
		_			90	•				95					100	. 4	
25	Tro	Tro	Trp	Ser	Leu	Leu	Lys	Glu	Glv	Ara	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
							- ;		•					_			
			•				٠,										
30																	
												•					
					*							0					- 1
35								-		- 0							

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5			105					110		٠			115				
	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu
	120					125					130					135	
10	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
				140					145					150		٠.	•
	Tyr	Туг	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
15		155					160					165		·			17.0
	Ala	Pro	Arg	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
					175					180					185		
20	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
			190					195					200				
	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
25	205					210					215					220	
	Val	Val	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
			-	225		÷	·,	_	230					235			
30	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240		•			245					250					255
35	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
÷					260	•				265					270		
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
40			275					280					285				
•	Asp	Val	Asp	Arg	Val	Leu	Va1	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	290		•			295					300					305	
45	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	qeA	Tyr	Gln	Asp	Met	Ile
				310					315					320		<del>.</del>	
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
50		325	٠			٠.	330					335					340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly.
					345					350					355		

5	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Туг
			360				•	365					370				
	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg
10	375					380		· · ·			385					390	
	Arg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
				395					400		•			405			
15	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410					415		.*			420					425
••	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
20					430				**	435				-	440		
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp
<b>25</b> .	•		445	:.				450					455	•			
	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460			,		465		j - `		. • • •	470	•				475	-
30	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
	•			480					485	•	•			490			
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
35		495					500			"		505	· ~- `	••••			510
	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
	÷				515		12			520			•		525		
40	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
			530	•				535					540				
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
45	545					550					555					560	٠
	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
	•		•	565				÷	570		•			575			
50	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
		580					585				٠	590					595
•	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro

_					600					605		•			610			
5	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr	
	. ;		615		•			620					625					
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	Asp	Arg	Arg	Ala	Ala	Leu	
10	630					635					640					645	•	
	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr	
				650					655					660		•		
15 -	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu	
		665			•		670					675			٠		680	
20	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His	
20					685					690					695	,		
	Leu	Leu	Ala	Phe	Asp	Arg	Gly	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu	
25			700				;	705					710					
	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	
	715					720	j.				725					730		
30	Ala	Val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe	
				735					740					745				
	Gly	Pro	Gly	Ala	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala	
35		750					755		-		'	760		e -·			765	
. =	Leu	Leu	Val	Pro	Gln	Thr	Gly	Gly	Glu	Ser					٠.			
				w.j.,	770			3 5		775								
40 🗥																		

21. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

SEQ ID NO:10:

45

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA 60
CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGC GGTGCCGATT CCGAACCCGT 120
GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG 180
CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC 240

5		
•	TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA	300
	GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA	360
10	GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC	420
	GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA	480
	CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGC	540
15	AGGCAAGCAG GGCGGGACGG GCTC	564
	ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC	612
	Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe	
20	1 5 10 15	
	ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG	660
	Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly	
25	20 25 30	
	GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC	708
	Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser	
30	35 40 45	
	GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC	756
	Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg	
35	50 55 60	
	GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC	804
	Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala	
40	65 70 75 80	
	GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG	852
	Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala	
45	85 90 95	
	TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC	900
	Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg	
50	100 105 110	
	GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG	948
	Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly	

5			115					120					125	5				
	GGC	CGC	ATC	CGG	ATC	ccc	GTC	CTG	GGC	AGC (	GAC G	AC G	SAT	CTG	GAC	CA	G	996
	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asg	Le	u As	sp (	Gln	
10		130	•	• .*			135	-				140			2	•		
	CTC	GAA	ATC	AAG	GAC	GGC	GAG	CTG	CGG	TAC 1	rac G	AC C	CAC	CGC	TTC	CC	G	1044
	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	a Ar	g Pi	ne I	Pro	•
15	145		٠		?	150		٠			155	•					160	
	CTG	GCC	GAG	GGC	AGC	TAC	CGG	GAC	GGC	GAC 1	rcc c	CG C	AG (	GAC	GTC	CA	С	1092
	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp	Ser	Pro	Glr	a As	p Va	al 1	His	
20		٠.			165					170				` ,	17	75		
	GGC	CGG	CAG	CAC	TAC	GAA	CTC	ATC (	GGC '	rgg c	CGG C	GC G	CC (	GAC	AAT	GA	A	1140
25	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	ı Ası	p As	sn (	Glu	
25				180		-			185					19	0			
	CTG	AAC	TAC	CGC	CGG	TTC	TTC	GCG (	GTG 2	AAC A	CG C	TC G	icc (	GC.	ATC	CG	G	1188
30	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gl	y Il	.e 2	Arg	
30			195	,				200					205	; ·			Tura.	
	GTG	GAG	GTG	CCG	CCG	GTC	TTC	GAT (	GAA (	GCG C	AC C	AG G	AG (	<b>GTG</b>	GTG	CG	Ċ	1236
35	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu	Va:	l Va	ıl	Arg	
		210				•	215					220						
	TGG	TTC	CGT	GCG	GGG	CTC	GCC	GAC (	GGG (	CTG C	GG A	TC G	AC C	CAC	CCG	GAG	3	1284
40	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	H1:	s Pr	O 7	Asp	
-	225					230	•				235					. 2	240	
	GGC	CTG	GCC	GAT	CCC	GAG	GGG	TAT :	rtg i	AAG C	GG C	TC C	GT (	GAG (	GTC	ACC	3 .	1332
45	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Gli	ı Va	1.1	Thr	,
					245			ē		250					25	5		
	GGG	GGC	GCG	TAC	CTG	CTC .	ATC	GAA /	AAG A	ATC C	TC G	AG C	CG C	GC (	GAA	CAC	3	1380
50	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	, Gl	u C	Gln	
				260					265					270	)			•
	TTG	CCG	GCC	AGC	TTC	GAG '	TGC	GAA (	GC A	ACC A	CC G	GC T	AC G	SAC (	GCC	CTC	3	1428

5					·											٠.	
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	- -
			275					280					285				
10	GCG	GAT	GTC	GAC	AGG	GTC '	TTC (	GTG (	GÀC C	cc c	GG G	GA C	AG G	TG C	CG CT	G :	1476
	Ala	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	
		290					295					300					
15	GAC	CGT	CTG	GAC	GCA	CGG	CTG	CGC (	GGC (	GT G	CG C	CG G	CC G	AC T	AC GA	.G	1524
							•		•						Tyr		
	305			15.	•	310					315			•		320	
20		ATG.	-			ACC	AAG	CGC	CGG 1	ATC - A	CC G	AC C	GC A	TC C	rg ca	.c.	1572
20		-	•												Leu		
				. •	325					330					335		_
25	TCC	GAG	ATC	CTG	CGC	CTT	GCC	AGG	CTG (	STG C	cc o	GAG (	CAG A	CC G	GA AI	'T	1620
															Gly		
	, 55-	-		340					345	•				350	• •	٠٠٠.	
30	ccc.	GGG	GAG	GCG	GCC	 GCG	GAT	GCG	ATC (	GCG (	GAG A	ATC 2	ATC G	CG G	CC TI	rc	1668
30															Ala		
		<b>-</b> _1	355				-	360		•			365		<b>-</b> .	Comp	
35	CCG	GTC			TCC	TAT	CTT	ccc	GAG	GGC (	GCG (	GAG A	ATC C	TG A	AG G	AG	1716
33															Lys		
		370	•	, <b>s</b>			375			•		380					
40	ccc			CTC	GCC	GCG	CGG	AGG	CGT	CCG (	GAA (	CTG (	GGC (	CAG A	.CC G1	rc	1764
40								,							Thr		
	385		, voř			390			, ,		395			•	•	400	٠
			CTC	CAG	cce			CTG	GAT	ACC (			GAG 1	ATT I	cc c	GC	1812
45															Ser		
	GIN	Leu	Leu	I GLI			ı bec	ı bet	, not	410		•			415		•
					405		CCA	አመሮ	CTC		•		GGC (	STG G		AC	1860
50													•		GAG G		
	Arg	Phe	Glr			r ser	. GI	Me1			, MIS	, ny:	, <u>u.</u> ]	430	. Glu		
				420	) .				425	)				-100	•		

5	ACC	GCG	TTC	TTC	CGC	TAC	AAC	CGG	CTG	GGA A	.cg c	TC AC	CC GA	AG G	TG GG	С	1908	
	Thr	Ala	Phe	Phe	Arg	Туг	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly		
		: ;	435	شدف	<u> </u>			440	. 3 5	.2			445				:	
10											AG G	AG T	rt C	AC G	rc cg	G	1956	
	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu	Glu	Phe	His	Val .	Arg		
		450			<u>.</u>		455					460						
15	ATG	GCC	CGC	CGG	CAG	GCC	GAA	CTC	CCG	CTC T	CC A	TG AC	CC AC	CC C'	TG AG	С	2004	
	Met	λla	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser		
	465		ar T	r si	.5 .41	470	٠ ــــــــــــــــــــــــــــــــــــ	. ~			475					480	at A	
20	ACG.	CAC	GAC	ACC	AAG	CGC	AGC	GAG	GAC	ACC C	GG G	cc c	GG A	TC T	CG GT	G Z	2052.	25
:	Thr	His	Asp	Thr	. Lys	. Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	GR.	
					<sub>2</sub> 485		·			490			. ~,	: 1 g	495	7.4. J	de.	
25.	ATC	GCC	GAG	GTC	GCG	CCT	GAA	TGG	GAA	AAG G	cc c	TG G	AC AC		rg aa		2100	25.
•	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg	Leu	Asn		
				500					505					510				
30	ACC	CTC	GCT	CCG	CTG	CCG	GAC	GGC	ĊCG	стс т	CC A	.cg c	rg C	TC T	GG CA	G	2148	::
	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu :	Leu	Trp	Gln		
			515					520	)		· ·		525	-			. (	
35	GCG	ATT	GCG	GGG	GCA	TGG	CCG	GCC	AGC	ccc c	AA C	GC C	TT C	AG T	CC TA	c	2196	
	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser '	Tyr		
		530	•				535					540						
40	GCC	CTG	AAA	GCG	GCG	CGC	GAA	GCC	GGG	AAC T	CG A	CC AC	SC TO	GG A	CC GA	T <sub>.</sub>	2244	
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp		
	545		•			550					555				at Si	560		
45	CCG	GAC	CCG	GCA	TTC	GAG	GAG	GCA	CTT	TCC G	ICC G	TC G	rc G	AC TO	CC GC	c a	2292	
•	Pro	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	λla	40.	··· •·· .
<b>5</b> 0		:			 565	t		·		570				·	575		*	
50	TTC	GAC	AAT	CCG	GAG	GTG	CGT	GCG	GAA	CTT G	ÄG G	CC CI	rg gi	TG G	GC CT	С	2340	
•	Phe	Asp	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu		

5	: .				580					585					590	)	•	****	
	c	CTT	GCG	ĊCG	CAC	GGT	GCG	TCC	AAC '	TCG (	CTC (	GCG (	GCA A	AG C	TT (	STC	CAG	- 238	8
	I	Leu	Ala	Pro	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Lev	ı Va	1 G1	.n	
10	* : •	* _		595	- 64	,			600					605					
	C	CTG	ACC	ATG	CCG	GGC	GTT	CCG	GAC	GTG '	TAC	CAG	GGC A	CC G	GAG 1	TTC	TGG	243	36
	I	Leu	Thr	Met	Pro	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	ı Ph	e Tr	p	
15		•	610	, ~-				615			•		620						
	C	GAC	AGG	TCG	CTG	ACC	GAT	CCG	GAC	AAC (	CGG (	CGC .	CCC 1	TC A	AGC 1	rtc	GCC	248	14
	7	Asp	Arg	Ser	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	. Ph	e Al	.a	
20	. 6	525	.,				630					635	<b>i</b>	•	•	•	64	10	
	C	GAA	CGG	ATT	AGG	GCC	TTG	GAC	CAG	TTG	GAC (	GCC	GGC C	CAC C	GT (	CCG	GAC	253	32
	. (	31u	Arg	Ile	Arg	Ala	Leu	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	7 Pr	o As	sp.	
25	. *-	*,**			•	645	•	,	٠		650			•	,•	65	5		
	•	rcc	TTC	CAG	GAC	GAG	GCG	GTC	AAG	CTG	CTG (	GTC .	ACC 1	rcg A	AGG (	GCG	CTG	258	30
	. 5	Ser	Phe	Gĺn	Asp	Glu	Ala	Val	Lys	Leu	Leu	Val	Thr	Ser	Arg	Al	a Le	eu.	
30				•	660				•	665	-,		-		670	כ (	44.		
		CGG	CTG	CGG	CGG	AAC	CGG	ccc	GAG	CTC	TTC .	ACC'	GGC 1	rac (	CGC (	CCC	GTG	262	28
35	1	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Aro	g Pr	o Va	al	
<b>-</b> ,				675					680					685					
	•	CAT	GCC	AGG	GGC	CCC	GCC	GCC	GGG	CAC	CTG (	GTG	GCG 1	rtc (	GAC (	CGC	GGC	267	76
40	. 1	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His	Leu	\Val	L Ala	Phe	. Ası	p Ax	g G	ГĀ	
			690			•		695					700			*# :	•		
													ccc 1						24
45	i	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg	Lei	Pro	Tyr	Gly	y Le	u G	lu	
		705		•			710			•		715					`73		
*	(	CAG	TCG	GGC	GGC	TGG	CGG	GAC	ACC	GCC	GTC	GAG	CTT (	GAA (	GCC (	GCC	ATG	27	72
50	. (	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	. Glu	Leu	Glu	Ala	a Al	.a Me	et	
						725					730		: :		٠٠	73			
	i	ACG	GAC	GAA	CTG	ACC	GGC	TCC	ACT	TTC	GGG	CCG	GGA (	CCG (	GCG	GCG	CTG	28:	2C

	Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu	
5	740 745 750	
	TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868	
	Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr	
10	755 760 765	
	GGA GGC AAG TCA 2880	
	Gly Gly Lys Ser	
15	770	
	TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936	
20		
25	SEQ ID NO:11	
	GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTCGGTG 60	•
	GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120	
30	GACGTGAACT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180	
	CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240	
	TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300	
35	CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360	
	CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCGAGCCG 420	
	GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480	
40	GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540	
	CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600	
	GCGGAAAAGC CGGCGCCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660	
45	CCCGCTGGGG AGGACGC 677	
	ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725	
	Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe	
50	1 10 15	
	ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773	
	Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly	
55	20 25 30	

5	GTC	GAC	TGG	GTC	TAC	СТТ	TCT	CCG	GTC	CTG 2	ACT (	GCC (	GAG C	CAG C	GC T	CC	821
	Val	Asp	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	
		٠	35					40					45				
10	GAC	CAC	GGG	TAC	GAC	GTC	ACC	GAT	CCC	TCC (	GCC (	GTC (	GAC C	cc c	SAA C	GC	869
	Asp	His	Gly	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	
		50					55					60					
15	GGC	GGG	CCG	GAG	GGC	CTC	GCG	GCG	GTT	TCC 2	AAG (	GCG (	GCC C	GC G	SCC G	CG	917
	Gly	Gly	Pro	Glu	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	
	65		•			70		,			75		-			80	
20	GGC	ATG	GGC	GTG	CTG	ATC	GAC	ATC	GTG	ccc i	AAC (	CAC	GTG G	GC C	STC G	CG:	965
	Gly	Met	Gly	Val	Leu	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	
					85					90					95	·	د ماء
25	ACG	CCG	GCG	CAG	AAC	ccc	TGG	TGG	TGG '	TCG (	CTG (	CTC A	AAG G	AG G	GA C	GC	1013
	Thr	Pro	Ala	Gln	Asn	Pro	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	
				100			· <u>.</u>	•	105					110	)		:
30	CAG	TCC	CGT	TAC	GCG	GAG	GCG	TTC	GAC	GTC (	GAT :	rgg (	GAC C	TC G	CC G	GG	1061
•	Gln	Ser	Arg	Tyr	Ala	Glu	Ala	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	
			115			٠.		120				وم	_125				1
35	GGA	CGC	ATC	CGG	CTG	CCG	GTG	CTC	GGC .	AGC (	GAC (	GAT C	GAC C	TC C	SAC C	AG	1109
	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	19
40		130					135	;				140	1				
40	CTC	GAA	ATC	AGG	GAC	GGG	GAG	CTG	CGG	TAC ?	rac (	GAC (	CAC C	GA I	TC C	CG	1157
÷	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	Arg	Phe	Pro	
45	145					150	•				155	i				160	·, ·.
	CTC	GCC	GAG	GGA	ACC	TAC	GCC	GAA	GGC (	GAC (	GCC (	CCG (	CGG G	AT G	TC C	AC	1205
	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp	Ala	Pro	Arg	Asp	Val	His	· · :
50					165					170	•				175		
-	GCC	CGG	CAG	CAC	TAC	GAG	CTC	ATC	GGC '	TGG (	CGC (	CGC (	GCG G	AC A	AC G	AG	1253
	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Asp	Asn	Glu	

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5																	
3				180					185	. **	-	*	. •	190			
	CTG	AAC	TAC	CGC	CGC	TTT	TTC	GCG	GTG .	AAC .	ACG	CTC G	CC G	GC G	TC C	GC	1301
10	Leu	Asn	туг	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thi	: Leu	Ala	Gly	Val	Arg	
70			195		• *		•. •	200	. :	* .	-8		205				
	GTG	GAA	ATC	CCC	GCC	GTC	TTC	GAC	GAG	GCA	CAC	CAG G	GAG G	TG G	TG C	3C	1349
45	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	s Gln	Glu	Val	Val	Arg	٠
15		210					215	i		<b>.</b> .		220				•	
	TGG	TTC	CGC	GAG	GAC	CTT	GCG	GAC	GGC	CTG	CGG	ATC G	CAC C	CAC C	CG G	AC	1397
20	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	ı Arg	j Ile	Asp	His	Pro	Asp	809
20	225				-	230				٠, ٠٠.	23	5				240	.:·
	GGC	CTC	GCT	GAC	ccc	GAG	GGG	TAC	CTG	AAG	CGA	CTC.	GG G	AA G	TC A	cc	1445
25	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Lev	Lys	a Ar	g Leu	Arg	Glu	Val	Thr	
•		-		•	245					250	)				255		
	GGC	GGC	GCT	TAC	CTG	CTG	ATC	GAA	AAG	ATC	CTG	GAG (	CCG (	GG G	AG C	AG	1493
30	Gly	Gly	Ala	Тух	Leu	Leu	Ile	e Glu	Lys	; Ile	a Le	u Glu	Pro	Gly	Glu	Gln	,
				260					265	5 .		•		270			
	CTG	ccc	GCC	AGC	TTC	GAG	TGT	GAA	GGC	ACC	ACA	GGC 1	rac (	GAC G	cc c	TC	1541
35	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	G13	Th	r Th	r Gly	Туг	Asp	Ala	Leu	
			275					280	)				285	5.			
	GCC	GAC	GTC	GAC	CGG	GTT	CTC	GTG	GAC	CCG	CGC	GGC (	CAG (	GAA C	CG C	TG	1589
40	Ala	Asp	Val	. Asp	Arg	Val	Lev	ı Val	Ası	Pre	o Ar	g Gly	Glr	ı Glu	Pro	Leu	
		290					295	5				300	)				
	GAC	CGG	CTT	GAC	GCG	TCC	CTG	CGT	GGC	GGC	GAG	CCC	GCC (	GAC 1	TAC C	AG	1637
45	Asp	Arg	Leu	Asp	Ala	Ser	Le	Arg	g Gly	7 G1	y Gl	u Pro	) Ala	Asp	Туг	Glņ	
											31					320	
	GAC	ATG	ATC	CGC	GGA	ACC	AAG	CGC	CGG	ATC	ACC	GAC	GGT .	ATC (	CTG C	AC	1685
50	Asp	Met	Ile	Arg	Gly	Thr	Lys	s Arg	j Arg	g Il	e . Th	r Ası	G13	, Ile	. Leu	His	
					325	; ·				. 33	0	٠.			335		
	TCG	GAG	ATC	CTG	CGG	CTG	GCC	CGG	CTG	GTT	CCG	GGC	GAC	GCC I	AAC G	TT	1733

										•							
5	Ser	Glu	Ile	Leu	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	
				340					345					350		•	
	TCA	ATC	GAC	GCC	GGA	GCC	GAC	GCT (	CTC C	SCC G	AA A'	TC A	TC G	CC G	CC TI	rc	1781
10	Ser	Ile	Asp	Ala	Gly	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	
			355			-		360		•			365				
	CCG	GTC	TAC	CGC	ACC	TAC	CTG	CCG (	GAG (	GC G	CC G	AG G	TC C	TG A	AG GA	AG	1829
15	Pro	Val	Tyr	Arg	Thr	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	
		370					375					380		•	•		
	GCG	TGC	GAG	CTT	GCC	GCG	CGT	AGG (	CGG (	CCG G	AA. C	TC G	AC C	AG G	CC A1	rc	1877
20	Ala	Суз	Glu	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	
	385					390			. •		395				• :.	400	CF7
	CAG	GCT	CTG	CAG	CCG	CTG	CTG	CTG (	GAC A	ACG G	AC C	TC G	AG C	TȚ G	cc co	GG <sub>.</sub>	1925
25	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	
	· , •	į	• • •		405			j ·		410					415		
20	CGC	TTC	CAG	CAG	ACC	TCG	GGC	ATG	GTC 2	ATG G	CC A	AG G	GC G	TG G	AG G	AC	1973
30	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	
			٠	420		•			425					430			•
35	ACC	GCG	TTC	TTC	CGC	TAC	AAC	CGC	CTG (	GGC 1	rČC C	TC A	.CG -G	AA G	TG G	GC .	2021
: ·	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
			435			•		440	•		•		445				
40	GCC	GAC	CCC	ACC	GAG	TTC	GCC	GTG	GAG (	CCG (	SAC G	AG T	TC C	AC G	CC C	3G	2069
	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp	Glu	Phe	His	Ala	Arg	
•		450					455					460					
45	CTG	GCA	CGC	CGG	CAG	GCC	GAG	CTT	CCG	CTG 1	rcc a	TG A	CG A	.CG C	TG A	GC	2117
	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	
	465	•	• •			470					475					480	
50	ACG	CAC	GAC	ACC	AAG	CGC	AGC	GAG	GAC .	ACC (	CGA G	CA A	.GG A	T T	CG G	TC	2165
	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
					485	i				490					495		

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5	ATT	TCC	GAG	GTT	GCG	GGT	GAC	TGG	GAA .	AAG (	scc :	TTG A	AC C	CGG C	TG C	GC	2213
	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg	Leu	Arg	1
	•			500					505					510			~
10	GAC	CTG	GCC	CCG	CTG	CCG	GAC	GGC	CCG	CTG 1	rcc o	GCG C	TG C	TC T	GG C	AG	2261
	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp	Gln	ı
			515					520				-	525				•
15	GCC	ATT	GCC	GGC	GCC	TGG	ccc	GCC	AGC (	CGG G	SAA (	CGC C	TG C	AG T	AC T	AC	2309
	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr	
		530					535					540				i.r.	
20	GCG	CTG	AAG	GCC	GCG	CGT	GAA	GCG	GGG 2	AAC I	CG 1	ACC A	AC T	GG A	CC G	galak AŢ	2357
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	200
	545					550					555		_	•		560	- 15°
25	CCG	GCC	ccc	GCG	TTC	GAG	GAG	AAG	CTG /	AAG G	CC G	CG G	TC G	AC G	CC G	TG	2405
	Pro	Ala	Pro	Ala	Phe	Glu	Gļu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	
			-		565		·'.			570	·				575		
30	TTC	GAC	AAT	ccc	GCC	GTG	CAG	GCC (	GAG (	TG G	AA C	cc c	TC G	TC G	AG C	TC .	2453
	Phe	Asp	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	ė
				580					585					590-	1 = 1, 1 441		
35	CTG	GAG	CCG	TAC	GGA	GCT	TCG	AAC '	rcc c	CTC G	CC G	CC A	AG C	TC G	TG C	AG	2501
	Leu	Glu	Pro	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	
40			595		•			600			,		605	•			
••	CTG	ACC	ATG	CCC	GGC	GTC (	CCG (	GAC (	STC 1	AC C	AG G	GC A	CG G	AG T	rc T	3G	2549
	Leu	Thr	Met	Pro	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	•
45		610					615					620				• -	
	GAC	CGG	TCG	CTG	ACG (	GAC (	CCG (	GAC A	AAC C	GG C	GG C	CG T	TC A	GC TI	rc G	AC	2597
	Asp	Arg	Ser	Leu	Thr	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	
50	625					630			-		635					640	
	GAC	CGC	CGC (	GCC	GCG (	CTG (	GAG (	CAG (	CTG G	AT G	CC G	GC G	AC C	TT C	CC GC	CG	2645
	Asp	Arg	Arg	Ala	Ala	Leu	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	

zc

12.5

5					645					650					65	5	
	TCA	TTT	ACC	GAT	GAG	CGG	ACG	AAG	CTG	CTA G	TG A	CG T	CG C	GC 0	CG (	CTG - 2	2693
	Ser	Phe	Thr	Asp	Glu	Arg	, Thr	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	a Lev	ı
10				660					665					670	<b>)</b>		
	CGG	CTG	CGC	CGG	GAC	CGT	CCG	GAG	CTG	TTC A	CG G	GG T	'AC C	GG (	CG	GTC	2741
	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	val	
15			675					680					685				
	CTG	GCC	AGC	GGG	CCC	GCC	GCC	GGG	CAC	CTG C	TC G	CG T	TC G	AC C	GC (	GC	2789
	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His	Leu	Leu	Ala	Phe	Asp	Arg	Gly	
20		690					695					700			. •		17 - 4 - 4
	ACC	GCG	GCG	GCG	CCG	GGT	GCA	TTG	ACC (	CTC G	ECC A	.CG C	GG C	TT C	cc '	PAC	2837
26	Thr	Ala	Ala	Ala	Pro	Gly	, Ala	Leu	Thr	Leu	Ala	Thr	Arg	Leu	Pro	тут	·
25	705		•			710	)				715					720	)
	GGG	CTG	GAA	CAG	TCG	GGT	GGA	TGG	CGG	GAC A	CC G	CC G	TC G	AA C	TT Z	AAC	2885
30 ·	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu	Lei	ı Aşr	
			•		725		•			730					73!	5	
	ACC	GCC	ATG	AAA	GAC	GAA	CTG	ACC	GGT (	GCC G	GC 1	TC G	GA C	CG (	GG (	GCA	2933
35	Thr	Ala	Met	Lys	Asp	Glu	. Leu	Thr	Gly	Ala	Gly	Phe	Gly	Pro	Gly	y Ala	
				740			•		745					750	)		
	GTG	AAG	ATC	GCC	GAC	ATC	TTC	CGG	TCG	TTC C	cc é	TT G	CG C	TG C	CTG	GTG	2981
40	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala	Lev	Le	ı Val	
			755				,	760				•	765	•			ž.
	CCG	CAG	ACA	GGA	GGA	GAG	TCA			•							3002
45	Pro	Gln	Thr	Gly	Gly	Glu	Ser									.,-	٠. ٠
•		770					775					٠.					
	TGAC	CGCA	CAC	TACC	CGCC	G G	AAGCC	GCGA	AAC	CCGTC	CT G	GGCC	CCGC	A CO	CTA	CGACG	3062
50	TCTC	GGC	GCC (	3													3073

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22. The transformant as claimed in claim 16, wherein said DNA is derived from a microorganism selected from the group consisting of the genera Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium and Terrabacter.

- 23. The transformant as claimed in claim 16, wherein said self-replicable vector is a plasmid vector Bluescript II SK(+).
- **24.** The transformant as claimed in claim 16, wherein said host is a microorganism of the spices *Escherichia coli*.
  - 25. A recombinant enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.
- 10 26. The recombinant enzyme as claimed in claim 25, which has the following physicochemical properties:
  - (1) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PA-GE); and

(2) Isoelectric point (pl)

About 3.6-4.6 on isoelectrophoresis.

27. The recombinant enzyme as claimed in claim 25, which has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

<sup>25</sup> 1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

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			20					25					30				
	Trp	Ile	Tyr	Leu	Ser	Pro	Ile	Leu	Lys	Ala	Glu	Ser	Gly	Ser	Asp		GIY
10	35					40					45			-		50	
	Tyr	Asp	Val	Thr	Asp	Pro	Ala	Val	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
90				55					60			•		65			
45	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Gly	Ala	Gly	Met	Gly	Val	Leu
15		70					75					80					85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Ser	Pro	Pro	Gln	Asn	Pro
20					90					95					100	7 1	
20	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gly	Ser	Pro	Tyr	Ala	Val	Ala
	• •		105					110		:			115			- : -	7 .
25	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu
25	120					125					130				:	135	
	Gly	Ser	. Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg
30 ·	-			140					145					150			
	Tyr	Туг	. Ast	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	, Asp	Gly	Asp
		155	_				160					165			•	:.	170
35	Ser	Pro	Glr	Asp	. Val	His	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	e Gly	Tr	Arg
<b>J</b> J					175					180				·.	185	_	
	Arc	, Ala	a Ası	) Asr	. Glu	Leu	Asr	Tyr	Arg	Arg	g Phe	e Phe	Ala	va:	l Asr	Thi	Leu
40			190					195			•		200				
	Ala	a Gl	y Ile	e Arg	y Val	Glu	val	Pro	Pro	va:	l Phe	e Ası	Glu	ı Al	a His	s Gl	n Glu
·	205					210		•			21	_				220	
45	Va:	l Va	l Ar	g Tr	p Ph∈	Arç	, Ala	a Gly	Le	ı Al	a As	p Gly	y Lei	ı Ar	g Il	e As	p His
45				22!					23					23			
	Pro	o `As	n Gl	y Le	u Ala	a Ası	Pr	o Gli	ı Gl	у Ту	r Le	u Ly	s Ar	g Le	u Ar	g Gl	u Val
<b>5</b> 0		24		_			24			•		25					255
50	ሞኮ			y Al	a Tyi	c Lei	ı Le	u Ile	e Gl	u Ly	s Il	e Le	u Gl	u Pr	o G1	y Gl	u Gln
	4.4		·4	•	260					26					27		

5																	
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp		_	
			275		٠.	-		280				÷.	285				i
10	Asp	Val	Asp	Arg	Val	Phe	Val	Aśp	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
70	290		. "		•	295	ī.; ·				300	-	7	• •		305	: :
	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	Asp	Met	Ile
15			•	310					315	:	•		•	320			
73	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325					330					335			٠.,		340
20	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
20					345					350				د. ۔	355	uo:	H
	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
25			360					365	٠			;;; <u>-</u>	370	• •	🗧 🗸	iew y	ZIO
	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	λla	Cys	Asp	Leu	Ala	Ala	Arg
	375	-		: .	,	380	į				385			7	• 1	390	: •
30	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
		٠.		395			: '		400					405	• •	٠.	
	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	-Gly	Met	Val
35		410			-		415	<u> </u>	() <b>-</b>			420	*		-		425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
					430	**				435					440		
40	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
			445				٠.	450					455		•		•
	Glu	Phe	His	Val-	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Lėu	Ser	Met
45	460		,			465					470			-	·. :	475	
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
	٠		ż	480					485			٠, ٠		490	· · ·	ī _	1L
50	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg
		495			•	: :	500		••	•		505			-		510
	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu-	Leu	Trp

							•		•								
5					515	•				520		: .			525		
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	тут
			530					535				-	540			•	• .
10	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545					550				٠	555					560	
	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
15				565					570					575			
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
		580		•			585					590					595
20	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
					600					605	:		:		610	avi t	:
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thi
25			615		•		:	620					625		:: <sub>   </sub> :	: *	æ i
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Let
••	630		•			635		•			640		·-	•		645	
30	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Glu	Ala	Va]
				650					655					660			
35	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
	•	665					670					675					680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
40		•		•	685		÷ * *			690				•	695		
	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
			700					705		••			710		٠.		
45	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glı
	715					720					725					730	
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gl
<b>50</b> ·				735					740					745			
	Pro	Ala	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Va]
	•	750					755				_	760					765

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# Pro Ala Thr Gly Gly Lys Ser 770

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													•				
5	SEQ	ID N	10:4														
	Met	Arg	Thr	Pro	Val	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Lys	Gly	Phe	Thr
	1				5					10					15		
10	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	Val	Asp
			20					25					30				
15	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gl
	35					40					45					50	
	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
20				55					60					65			
	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Let
	٠	70					7.5					80	•				85
25	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
					90					95					100		
	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
30			105					.110					115				
	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Leu	Pro	Val	Le
	120		-			125				.:	130			į .		135	
35	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
				140					145					150	•		
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	G1u	Gly	Thr	Tyr	Ala	Glu	Gly	Ası
40		155					160					165					170
	Ala	Pro	Arg	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Ar
		:			175					180					185		
45	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Le
			190					195		-			200				

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Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu

5																		
	. 20	5	•				210					215					220	
	Ve	al	Val	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
10		٠.			225					230					235			
	Pı	0	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		• :	240	•				245					250					255
15	Tì	ır	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	G1ú	Pro	Gly	Glu	Glr
	• '					260					265					270		
	Le	eu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
20				275				•	280					285			-	
	. As	sp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	29	90			•		295					300				•	305	
25	Le	eu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
					310					315			•		320			
	A	rg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Let
30			325	•				330					335				·	340
	A	ŗg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gl
	•					345		÷			350					355		٠.
35	<b>A</b> .	la	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Тул
				360					365					370				
	Le	∋u	Pro	Glu	Gly	Ala	Glu	Val	Leu	Ļys	Glu	Ala	Суѕ	Glu	Leu	Ala	Ala	Arc
40		75					380		•			385			•		390	
	A	rg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu 	Leu	Leu
					395					400					405		•	
45	A:	ge	Thr	Asp	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Gln	Gln	Thr	Ser			
			410					415					420				( :**·	
	Me	et	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn		Leu	G17
50						430					435					440		
	T	nr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Ası
				445					450					455	•	-		

5																	
	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460					465					470		•:			475	
10	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480					485	٠.				490			
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
15		495					500					505					510
,,	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
		•			515					520					525		
20	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
			530				-	535					540				
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
25	545					550					<b>555</b> .				· :	560	ن.
	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
				565		•	· į		570			÷		575			
30	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
		580		•	•		585					590				<b></b>	595
	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
35					600					605	+ 5 **		-		610		
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
			615					620					625	•			
40	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	Asp	Arg	Arg	Ala	Ala	Leu
	630					635	2°				640				÷	645	
	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr
45				650					655	•				660			
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu
		665					670					675					680
50	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His
					685	,				690					695		
	Leu	Leu	Ala	Phe	Asp	Arg	Gly	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu

			700					705					710					
										_						_		
5	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	
	715	5	• •	• •		720					725					730		
	Ala	val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe	
10				735					740					745				
	Gl	Pro	Gly	Aļa	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala	
		750	-		•	,	755					760	_				765	
15	Lev	ı Leu	Val	Pro	Gln	Thr	Gly	Gly	Glu	Ser								
	. •				770					775								
	7	; •														.,		
20	i																ble of form- sultant cul-	
25		The pro properti		s clain	ned in	claim	28, wh	nerein	said re	ecomb	inant e	enzym	e has	the foll	lowing	physi	cochemical	
		(1) M				ltone	00 800	dium d	odecu	d culfa	te poly	acryla	mida	aal ala	u :	: :3: horoole	s (SDS-PA-	
		GE);	and			110113		Jidili d	odecy	i Sulla	te puly	acı yı	iniue ;	gei eie	sctropi	ioi esi	S (SDS-FA-	
30			oelect t 3.6-4	•	,	ctroph	oresis		•	•	• •			*		-	·	
																	i sequence	
		selected ermina														itiate f	rom the N-	
35			, 1	-		6				- 40								
	SEC	ID	NO:2													-		
	Met	: Arg	Thr	Pro	Ala	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Arg	Gly	Phe	Thr	
40	1	•			5			٠.		10			•		15	•		
٠							•											

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5	Leu	Phe	Asp	Ala	Ala	Glu	Thr	Val	Pro	Tyr	Leu	Lys	Ser	Leu	Gly	Val	Asp
			20					25					30				
	Trp	Ile	Tyr	Leu	Ser	Pro	Ile	Leu	Lys	Ala	Glu	Ser	Gly	Ser	Asp	His	Gly
10	35					40					45					50	
	Tyr	Asp	Val	Thr	Asp	Pro	Ala	Val	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55	•				60					65			
15	Gly	Leu	Ala	λla	Val	Ser	Lys	Ala	Ala	Arg	Gly	Ala	Gly	Met	Gly	Val	Leu
		70					75					80					85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Ser	Pro	Pro	Gln	Asn	Pro
20			•		90				•	95			•		100		
	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gly	Ser	Pro	Tyr	Ala	Val	Ala
			105					110					115				
25	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu
	120		•	٠.	•	125	į		٠.		130					135	
20	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg
30				140					145					150			
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp
35		155					160	•	•			165				. *	170
	Ser	Pro	Gln	Asp	Val	His	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
		. :			175					180					185		
40	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
			190					195					200				
	Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
45	205	•				210					215					220	
	Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
		•		225					230					235		•	
<b>50</b> -	Pro	Asp	Gly	Leu	Ala	λsp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240				•	245					250					255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln

5					260		. , •			265					270		
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
	•		275					280					285				
10	Asp	Val	Asp	Arg	Val	Phe	Val	Asp	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
	290		÷			295					300					305	
	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	Asp	Met	Ile
15	•			310					315					320			
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325					330				,	335					340
20	Arg	Leu	Ala	Arg	Leu.	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
					345					350					355		
	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
25			360					365	•	٠			370				
	Leu	Pro	Glu	Gly	Ala	Glu	Įle,	Leu	Lys	Glu	Ala	Cys	Asp	Leu	Ala	Ala	Arg
	375				•	380	`				385					390	
30	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
		٠.		395		•			400				• .	405	-:		-
35	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410		. 1+			415			. '	•	420					425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
40					430					435					440		
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
			445	٠			•	450	•				455				
45	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460	,,				465			٠		470					475	-
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
50			•	480					485		•			490			
	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	rys	Ala	Leu	Asp	Arg
		495					500					505				:	510

5	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp
					515					520					525		
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr
10	•		530	··"				535		•			540				
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545			-		550			•		555					560	•
15	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
			•	565		•			570					575			
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu.	Ala	Pro
20		580	· ·.				585	:				590					595
	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
					600	*				605					610		-
25	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
		000	615		-	• •	•	620				•	625				
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
30	630					635				•	640				•	645	
	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	qeA	Glu	Ala	Val
25				650					655					660			
35	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	
		665					670					675					680
40	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala			His
••		•			685			` .		690					695		
	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
45			700					705					710				٠.
	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala		
	715					720					725					730	
50	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly
				735				•	740					745			
	Pro	Ala	Ala	Leu	Ser	Glu	va]	Phe	Arg	Ala	туг	Pro	val	. Ala	Leu	Lev	val

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		750					755					760					765
	Pro	Ala	Thr	Gly	Gly	Lys	Ser					-					
5				٠	770												
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10			. • .	•				•									
	SEQ	ID 1	NO:4													•	
15	Met	Arg	Thr	Pro	Val	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Lys	Gly	Phe	Thr
	1				5					10					15		
	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	Val	Asp
20			20					25					30				
	Trp	Val	Tyr	Leu <sup>.</sup>	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gly
	.35				•	40 -					45					50	
25	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55					60				•	65			
	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Leu
30		70					75		•			80					85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln.	Asn	Pro
					90					95					100		
35	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
			105	•				110	•				115		. ; ::		
	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu
40	120			•		125					130					135	
		Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
	. <u>-</u> .		•	140	_		_		145			_		150			
45	Tvr	Tvr	Asp		Ara	Phe	Pro	Leu		Glu	Glv	Thr	Tyr		Glu	Gly	Asp
•		155			3		160	•			2	165	•				170
	Δla		Ara	Asn	Va l	Hig		Ara	Gln	Hie	ጥህጕ		Leu	Ile	Gly	Tro	Ara
50					175			··- y	~~	180	-1-				185		3
	1-~	Ala	۸۵۸	Acn		Leu	Δες	Մերա	Ar~		Dha	Dhe	<b>1</b> 12	Va1		<b>ፐኮ</b> ታ	Lëu
	wrg	VTG		ASII	GIU	rea	ASN		Arg	wrg	rne	rne .		AGT	Asn		neu
55			190					195	•				200				

5																	
	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala	Val	Phe	qeA	Glu	Ala	His	Gln	Glu
	205					210					215					220	
10	Val	Val	Arg	Trp	Phe	Arg	Glu	qzA	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225					230			•		235			
	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
15	• •	240	• ;				245					250					255
,,	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
	÷ .	٠.	-		260					265					270		
20	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
		-	275					280				٠	285				, <u>.</u> .
	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
25	290	• .		į.		295					300			٠,		305	
	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
				310					315	,				320		٠	
30	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325				<u>-</u>	330					335					340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
35		*	J 181 *		345					350					355		
	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Tyr
			360					365				,	370				
40	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	rys	Glu	Ala	Cys	Glu	Leu	λla	Ala	Arg
	375					380					385					390	
	Arg	Arg	Pro	Gļu	Leu	Asp	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
45				395					400					405			
	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410					415					420					425
50	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Туг	Asn	Arg	Leu	Gly
					430					435		• .	• '		440		
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	geA
											•						

5			445					450					455				
	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460					465					470					475	
10	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480					485					490			
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
15		495	٠.				500					505					510
	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
					515					520					525		
20	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
			530					535					540	- •			
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
25	545					550				ı	555					560	
	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
			,	565				•	570				• *	575			
30	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
		580					585					590		-	-	ŧ.e.	595
35	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
33		•			600			÷		605	:				610	•	
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
40			615				•	620				-	625				
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	Asp	Arg	Arg	Ala	Ala	Leu
	630	•				635					640		•			645	•
45	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr
				650					655				;	660			
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu
50		665			•		670		•			675				•	680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His
					685		-		٠.	690			•		695		• •

	Leu	Leu	Ala	Phe	Asp	Arg	Gly	Thr	Ala	Ala	Ala	Pro	Ġly	Ala	Leu	Thr	Leu
5			700					705					710			er .n	
	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr
	715					720					725					730	
10	Ala	Val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Cly	Phe
				735					740					745			
	Gly	Pro	Gly	Ala	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala
15	•	750					755					760	•				765
	Leu	Leu	Val	Pro	Gln	Thr	Gly	Gly	Glu	Ser							
					770					775					. 427.	" its indi	
20			,											-	47. 637.	22 444	r lib

- 31. The process as claimed in claim 28, wherein said transformant is obtained by introducing into a suitable host a recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.
- 32. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequence to these base sequences:

### SEQ ID NO:1

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ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60
GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTCGCCC 120
ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
GACCCGGAGC GCGGCGCCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
GGCATGGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCGTGGCGTC GCCGCGCAG 300
AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360

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5 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420 GATCTGGACC AGCTCGAAAT CAAGGACGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540 10 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660 GAGGTGGTGC GCTGGTTCCG TGCGGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720 15 GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCACCGG GGGCGCGTAC 780 CTGCTCATCG AAAAGATCCT CGAGCCGGCC GAACAGTTGC CGGCCAGCTT CGAGTGCGAA 840 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA...900 20 CAGGTGCCGC TGGACCGTCT.GGACGCACGG CTGCGCGGCG GTGCGCCGGC.CGACTACGAG...960 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080 25 ATCGCGGAGA TCATCGCGGC CTTCCCGGTC TACCGGTCCT ATCTTCCCGA GGGCGCGGAG 1140 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACTGGG CCAGACCGTC 1200 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260 30 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320 CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380 TTTCACGTCC GGATGCCCG CCGCAGGCC GAACTCCCGC TCTCCATGAC CACCCTGAGC 1440 35 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500 GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCGGGGGCAT GGCCGGCCAG CCGGGAACGC 1620 CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680 CCGGACCCGG CATTCGAGGA GGCACTTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740 GAGGTGCGTG CGGAACTTGA GGCCCTGGTG GGCCTCCTTG CGCCGCACGG TGCGTCCAAC 1800 45 TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGGCG TTCCGGACGT GTACCAGGGC 1860 ACCGASTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCCTT CAGCTTCGCC 1920 GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980 50 GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGGCGGAA CCGGCCCGAG 2040 CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100

TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
CAGTCGGCCG GCTGGCGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACTG 2220
ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCGG 2280
GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA

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SEO ID NO:3

ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC 60 GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG: 120 GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC7:180 GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCGCAG 3300 AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT "420 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CCGGCAGCAC 540 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAG 660 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCGCTTAC 780 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900 CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTTCAA TCGACGCCGG AGCCGACGCT 1080 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140 GTCCTGAAGG AGGCGTGCGA GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380

TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CCGGGAACGC 1620 10 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680 CCGGCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTCG ACGCCGTGTT CGACAATCCC 1740 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800 15 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGGCG TCCCGGACGT CTACCAGGGC 1860 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980 20 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040 CTGTTCACGG GGTACCGGCC GGTCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100 TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160 25 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTCG AACTTAACAC CGCCATGAAA 2220 GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325 30

33. The process as claimed in claim 32, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ ID NOs:1 and 3 wherein one or more bases are replaced with other bases by means of degeneracy of genetic code without alternating their corresponding amino acid sequences as shown in the following SEQ ID NOs:2 and 4:

SEQ ID NO:2

45

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

50 35 40 45 50

5	туг	Asp	Val	Thr	Asp	Pro	Ala	Val	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55					60		•			65		±i£n,≵t.	- '
	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Gly	Ala	Gly	Met	Gly	Val	Leu
10	•	70					<b>75</b>		•			80					85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Ser	Pro	Pro	Gln	Asn	Pro
					90				,	95		٠			100		
15	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gly	Ser	Pro	Tyr	Ala	Val	Ala
			105					110					115				
	Phe	qzA	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu
20	120				• •	125					130			· ·	:	135	
	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg
				140					145					150		-	•
25	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp
		155		•			160					165			• •		170
	Ser	Pro	Gln	Ąsp	Val	His	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
30					175					180					185	•	
	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu 30
35			190				٠.	195	:				200				
	Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
	205					210			i		215					220	
40	Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225				٠.	230					235			
	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	
45		240					245					250					255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro		Glu	Gln
					260		÷			265					270		_
50	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275					280					285				
	Asp	Val	Asp	Arg	Val	Phe	Val	qzA	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg

5	290				··· .	295					300				-· • <del>-</del>	305	
	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu	Asp	Met	Ile
				310					315					320			r.
10	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325					330					335					340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
15			,		345					350					355		
	Ala	Asp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
			360		•			365					370	·	٠	<u>s</u> 7	
20	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys	Glu	Ala	Суѕ	Asp	Leu	Ala	Ala.	Arg
	375					380					385					390	
25	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
				395					400					405	·: .	: 5	'날 "
	Asp	Thr	qsA	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
30		410					415				•••	420					425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
		.,		• • • • • • • • • • • • • • • • • • • •	430.					435	•				440		
35	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
			445	= -		=		450					455				•
	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
40	460		:			465					470					475	
	Thr	Thr	Leu		Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp		_	Ala	Arg
				480					485					490	•		
45	Ile		Val	Ile	Ala	Glu		Ala	Pro	Glu	Trp		Lys	Ala	Leu		•
		495					500			٠.		505			: .		510
	Leu	Asn	Thr	Leu		Pro	Leu	Pro	Asp		Pro	Leu	Ser	Thr		Leu	Trp
50				_	515			•		520				_	525		
	Gln	Ala	Ile	Ala	Gly	Ala	Trp		Ala	Ser	Arg	Glu		Leu	Gln	ser	Ţyr
			530					535					540	•			

5	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	neA	Ser	Thr	Ser	Trp	Thr	Asp.	Pro
	545				•	550					555					560	·
	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
10				565	÷	•			570	•		*		575			•
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
		580					585			٠		590					595
15	His	Gly	Ala	Ser	Ąsn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
					600	-				605			•		610		
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
20			615					620				• .	625			; <del>4</del>	
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
	630					635					640		-	÷	. Ş	645	to s
25	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Glu	Ala	Va]
	•	÷		650	٠		·	•	655					660	• •	* *	*1
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
30		665	. •:	. •	<i>:</i>		670					675			+3+		680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
25		÷., ,			685	-			-	690					695		
35	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
			700		·			705	•				710	:			
40	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu
~	715					720		`,			725					730	
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gl
45			,	735			•	,	740		****		•.	745	•	-	
	Pro	λla	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Va]
		750					755	•		•		760					76
50	Pro	Ala	Thr	Gly	Gly	Lys	Ser										
-					770												

5	SEQ	ID 1	10:4		•				- 1	) : ,	··				-1	.e.	
	Met	Arg	Thr	Pro	Val	Ser	Thr	туг	Arg	Leu	Gln	Ile	Arg	Lys	Gly	Phe	Thr
	1			÷ •	5 .		: .			10	,				15		
10	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	Val	Asp
			20					25		- '- '			30				
	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gly
15	35					40			-		45					50	
	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55		. , .	<b></b>	: •• •	60	• 0	÷ :			65 .	; ]	ter je	
20	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Leu
		70			٠	. •	75					80 ;				.: :	85
	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
25					90			. :		95					100		±.1,
	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
			105		ja		÷ .	110					115			,	·.:
30	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu
	120					125					130					135	
	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg
35				140	- :				145					150			
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
		155					160		-			165	,				170
40	Ala	Pro	Arg	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
					175					180					185	:	
	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
45			190					195					200			•	÷
	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
	205			. •		210					215					220	
50	Val	Val	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225	•		•		230					235			

5	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
		240					245					250					255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
10					260					265					270		
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
			275					280					285				
15	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	290					295					300					305	
	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
20				310					315					320		机道	
٠.	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu.	His	Ser	Glu	Ile	Leu
-		325					330					335				٠.	340
25	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
					345					350					355	*	
	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Tyr
30		;	360					365					370			٠.	•
	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg
	375			•	* g	380	•				385					390	-;
35	Arg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
				395					400					405			
40	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
•	•	410					415				٠.	420					425
	Met	λla	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
45					430				:	435					440		
*	Thr	Leu	Thr	Glu	Val	Gly	Ala	qeA	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp
			445					450		•			455		•		,
50	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met
	460					465				•	470	•	•			475	,
	Thr	Thr	Leu	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg

5				480					485					490			
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
	•	495					500					505					510
10	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
					515					520					525		
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr
15			530					535	•	, · · ·			540				
	Ala	Leu		Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
	545		-			550					555					:5.60	
20		Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
				565			-		570				•	575			
	'Asn	Pro	Ala		Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
25	AG.	580					585					590		1			595
	Пата		 Δ1 a	Ser	Asn	Ser		Ala	Ala	Lvs	Leu	Val	Gln	Leu	Thr	Met	Pro
		GLy.	,	002	600	-	-j-	·:		605					610		. •
30	Glyr	17a1	Pro	Aen		TVT	Gln	Glv	Thr		Phe	Trp	Asp	Arg	Ser	Leu	Thr
	GIY	,	615	nap		-1-	0	620					625	J		z * .	
	3	D=0		a cn	Ara	`A+~	Pro		Ser	Phe	ASD	Asp		Arg	Ala	Ala	Leu
35	630				AL 9	635		•			640			3		645	
		C1-	T 011	3.55	<b>71</b> a		Aan	Len	Pro	λla		Phe	ሞከተ	Asp			Thr
	GIU	GIN	rea		VIG	GLY	vab	Deu	655	ALU	001			660		3	
40		• 🗀 .	•	650	Mb	<b>5</b> ~~	N	7 l a		) T.C	Leu	Ara	Ara	Asp	Ara	Pro	Glu
	ràs		rea	vaı	THE	Ser		VIG	nea	vrā	Deu	675	n.r.g		9		680
		665		<b>.</b>	<b>_</b> :	3	670	17-1	T	*1-	c		Pro	Ala	Ala	Glv	
45	Leu	Phe	Thr	GIA		Arg	PIO	vaı	reu		Ser	GIY	rio	VTG		011	His
					685					690		_	<b>01</b>		695	mb	T 011
	Leu	Leu		Phe	Asp	Arg	Gly		Ala	Ala	Ala	Pro		АТА	Leu	Thr	Leu
50			700					705					710				
	Ala	Thr	Arg	Leu	Pro	Tyr	ĠŢĀ	Leu	Glu	Gln		Gly	Gly	Trp	Arg		Thr
	715				•	720		٠.			725					730	

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	Ala	Val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe
_				735					740					745			
5	Gly	Pro	Gly	Ala	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala
		750					755					760					765
10	Leu	Leu	Val	Pro	Gln	Thr	Gly	Gly	Glu	Ser							. (-)
					770					775							

34. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

20	SEQ ID NO:10:	
	CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTC AAGCTCCCGT CGGATGAATA	60
	CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT	120
25	GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCCACAG	180
	CGCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC	240
	TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA	300
30	GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA	360
	GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC	420
	GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGCGAAG CCGGAAGAGG CTGCTTCCGA	480
35	CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGC	540
	AGGCAAGCAG GGCGGGACGG GCTC	564
	ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC	612
40	Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe	
	1 5 10 15	•
	ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG	660
45	Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly	
	20 25 30	
	GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC	708
<b>50</b>	Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser	
		····.
	35 40 45	

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5	GAC	CAC	GGĊ	TAT	GAC	GTC	ACC	GAT	CCC -	ecc o	GTA (	GTG (	FAC (	cce (	ĢAG	CGC	756
	Asp	His	Gly	Tyr	Asp	Val	Thr	Asp	Pro	Ala	Val	. Val	Asp	Pro	G1	u.Ärg	<b>3</b>
		50					55			-		60				- 1.2	<u>r</u>
10	GGC	GGC	CCT	GAA	GGG	CTG	GCC	GCG	GTG	TCC A	AAG (	GCG (	SCC (	CGC (	GGT	<u>ećc</u>	804
	Gly	Gly	Pro	Glu	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arc	g G1	y Ala	1
	65					70					75					80	
15	GGC	ATG	GGC	GTG	CTG	ATC	GAC	ATC	GTG	CCG A	AAC (	CAC C	etg (	GC (	GTG	GCG	852
	Gly	Met	Gly	Val	Leu	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gl	y Va	l. Ala	1
					85					90	:	<u>.</u> ; .		5	95	4,.°	
20	TCG	CCG	CCG	CAG	AAC	CCG	TGG	TGG	TGG '	TCG (	CTG (	CTC A	AG C	GAA (	GGG	CGC:	900
	Ser	Pro	Pro	Gln	Asn	Pro	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	ı Gl	y Arg	boa
				100					105					.110	) .3	<b>9.35</b>	7.1.D
25	GGG	TCG	CCC	TAC	GCC	GTG <sub>.</sub>	GCG	TTC	GAC (	GTC (	SAC :	rgg g	AC C	TG (	GCG	GGG	948
	Gly	Ser	Pro	Tyr	Ala	Val	Ala	Phe	Asp	Val	Asp	Trp	Asp	Leu	Al	a Gly	·
•			115				٠.	120					125	٠.		3 th T	э.
30	GGC	CGC	ATC	CGG	ATC	ccc	GTC	CTG	GGC 2	AGC G	SAC (	GAC G	ATC	CTG (	SAC	CAG	996
	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asp	Leu	As	p Gln	
35		130					135			=	-	140		.2	* =		
	CTC	GAA_	ATC.	AAG	GAC	GGC	GAG	CTG	CGG 1	rac t	'AC C	SAC C	AC C	GC 1	TC (	CCG	1044
	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	Arg	Phe	e Pro	1
40 -	145					150					155	٠.				160	ı
	CTG	GCC	GAG	GGC	AGC	TAC	CGG	GAC (	GGC (	SAC T	'CC C	CG C	AG G	AC G	TC (	CAC	1092
	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp	Ser	Pro	Gln	Asp	Va]	l His	
<b>1</b> 5					165					170		* **			175		
											•	GC G					1140
	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Asp	Asr	n Glu	
50				180					185					190			
												TC G					1188
	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gly	Ile	a Arg	

5			195					200	)				205	i			n.,
	GTG	GAG	GTG	CCG	CCG	GTC	TTC	GAT	GAA	GCG	CAC (	CAG (	GAG (	GTG	GTG	CGC	1236
	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu	ı Va	l Va	ıl Àr	g .
10		210					215				•	220					
	TGG	TTC	CGT	GCG	GGG	CTC	GCC	GAC	GGG	CTG	CGG 1	ATC (	GAC (	CAC	ĊCG	GAC	1284
	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	Hi:	s Pr	o As	p
15	225					230					235			-		24	.0
	GGC	CTG	GCC	GAT	CCC	GAG	GGG	TAT	TTG .	AAG	CGG C	CTC C	CGT (	GAG	GTC	ACC	1332
	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Туг	Leu	Lys	Arg	Leu	Arg	Gl	u Va	1 Th	i.i. I.E.
20		•			245		•			250	•				25	5	- Luci
	GGG	GGC	GCG	TAC	CTG	CTC	ATC	GAA	AAG .	ATC (	CTC G	GAG C	CCG (	GC	GAA	CAG	1380
25	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gl	y Gl	u G1	n martin
25	•			260					265					27	0		3,"2
	TTG	CCG	GCC	AGC	TTC	GAG	TGC :	GAA	GGC .	ACC .	ACC G	GC 1	TAC C	GAC	GCC	CTĆ	1428
30	Leu	Pro	Aĺa	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	As	p Al	a Le	iu 
			275			,	•	280					285	;			
										· :	CGG G						·
35	Ala	<u> </u>	Val	Asp	Arg	Val		Val	Asp	Pro	Arg	Gly	Gln	Va.	l Pr	o Le	u .
	•	290					295					300					
						٤					GCG C						1524
40	_	Arg	Leu	Asp	Ala	_	Leu	Arg	Gly	Gly	Ala	Pro	Ala	As	р Ту		
	305					310					315				ama	32	
											ACC G						1572
45	Asp	Met	IIe	Arg		Thr	Lys	Arg	Arg		Thr	Asp	GIY	. 116		::	
					325					330					33		1620
											CCC G					_	•
50	ser	GIU	тте		Arg	reu	ATS	Arg		val	Pro	GIU	GIN				•
	ccc	ccc	CAC	340	ccc	CCC /	C A CT	ccc	345		23C 3	.т.с. »	TC C	350 202		መመር	1668
		ناناب	GAG	فاناق	حرب	افاتان	GAT.	، فالاق	WIC (	<b>JUG</b> (	GAG A	IIC A	.10		ران	110	1000

5	Pro	Gly	Glu	Ala	Ala	Ala	Asp	Ala	Ile	Ala	Glu	ı Ile	Ile	Ala	Ala	Phe	
			355					360					365				
	CCG	GTC	TAC	CGG	TCC	TAT	CTT	ccc	GAG	GGC (	GCG	GAG A	ATC (	CTG A	AG G	AG	1716
10	Pro	Val	Tyr	Arg	Ser	Tyr	Leu	Pro	Glu	Gly	Ala	a Glu	Ile	Leu	Lys	Glu	
		370					375					380	)		•		
	GCC	TGC	GAC	ĊTC	GCC	GCG	CGG	AGG	CGT	CCG (	GAA	CTG (	GGC (	CAG A	CC G	TC	1764
15	Ala	Cys	Asp	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	ı Leu	Gly	Gln	Thr	Val	
	385					390					395	5				400	
	CAG	CTG	CTG	CAG	CCG	CTG	CTG	CTG	GAT .	ACC (	GAC	CTC (	GAG A	TT I	CC C	GC'	1812
20	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	
•					405					410	·				415		
	AGG	TTC	CAG	CAG	ACC	TCG	GGA .	ATG (	GTC	ATG (	SCC .	AAA (	GC G	TG G	AG G	AC	1860
25	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	5 "
				420			i		425	٠'				430	. ,		_
	ACC	GCG	TTC	TTC	CGC	TAC	AAC	ccc (	CTG (	GGA A	ACG (	CTC A	ACC G	AG G	TG G	GC	1908
30	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
			435		٠		•	440	٠				445		_	, aft or	
	GCC	GAC	CCC	ACC	GAG	ŤTC	TCG	CTG (	GAA (	CCG (	GAG (	GAG 1	TT C	AC G	TC C	GG -	1956
	Ala	Asp.	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu	Glu	Phe	His	Val	Arg	
		450					455				-	460					
40	ATG	GCC	CGC	CGG	CAG	GCC	GAA (	CTC (	CCG (	CTC I	CC 2	ATG A	CC A	cc c	TG AC	GC .	2004
40	Met	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	
	465					470					475					480	
45	ACG	CAC	GAC	ACC	AAG	CGC .	AGC (	GAG (	GAC A	ACC C	GG (	GCC C	GG A	тс т	CG G1	rg ,	2052
<b>~</b>	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
			•		485					490					495		
50	ATC	GCC	GAG	GTC	GCG	CCT (	GAA 1	rgg (	GAA A	AG G	cc o	CTG G	AC A	GG C	TG AA	VC.	2100
	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg	Leu	Asn	
				500					505		•			510			

5	ACC	CTC	GCT	CCG	CTG	CCG	GAC	GGC	CCG (	CTC I	CC A	.cg c	TG C	тс т	GG C	AG	2148
	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp	Gln	
			515	•				520				•	525		•		
10	GCG	ATT	GCG	GGG	GCA	TGG	CCG	GCC	AGC (	GG G	AA C	GC C	тт С	AG T	CC 1	'AC	2196
	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Tyr	
		530					535	i				540					
15	GCC	CTG	AAA	GCG	GCG	CGC	GAA	GCC	GGG 2	AAC I	CG A	CC A	GC T	GG A	CC G	AT	2244
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	
	545					550					555	:				560	
20	CCG	GAC	CCG	GCA	TTC	GAG	GAG	GCA	CTT :	rcc e	GCC G	TC G	TC G	AC T	CC G	CC	2292
	Pro	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	
	•		•		565					570					575	, <del></del>	
25	TTC	GAC	AAT	CCG	GAG	GTG	CGT	GCG	GAA (	CTT G	GAG G	cc c	TG G	TG G	GC C	TC	2340
	Phe	Asp	Asn	Pro	Glu	Val	Arg	, Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	
			-	580				`	585	٠.	•			590			
30	CTT	GCG	CCG	CAC	GGT	GCG	TCC	AAC	TCG (	CTC C	CG G	CA A	AG C	TT G	TC C	AG	2388
	Leu	Ala	Pro	His	Gly	Ala	Sex	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	. Gln	
25			595	·				600					605				
35	CTG	ACC	ATG	CCG	GGC	GTT	CCG	GAC	GTG .	TAC C	CAG G	GC A	.CC G	AG T	TC 1	'GG	2436
/	Leu	Thr	Met	Pro	Gly	Val	Pro	) Asp	. Val	Tyr	Ğln	Gly	Thr	Glu	Phe	Trp	
40		610	•			4	615	i	. "			620					
₩	GAC	AGG	TCG	CTG	ACC	GAT	CCG	GÀC	AAC	CGG C	CGC C	CC T	TC A	GC T	TC C	CC	2484
	Asp	Arg	Ser	Leu	Thr	Asp	Pro	) Asp	neA	Arg	Arg	Pro	Phe	Ser	Phe	Ala	
45	625					630					635					640	
	GAA	CGG	ATT	AGG	GCC	TTG	GAC	CAG	TTG (	GAC C	SCC G	GC C	AC C	GT C	CG	FAC	2532
	Glu	Arg	Ile	Arg	Ala	Leu	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	
50					645				•	650					655	j	
	TCC	TTC	CAG	GAC	GAG	GCG	GTC	AAG	CTG (	CTG (	STC A	CC T	CG A	GG G	CG (	CTG	2580
	Ser	Phe	Gln	Asp	Glu	Ala	Val	. Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	. Leu	

...

5				660				•	665					670		اسوالوپ سوالوپ	• .:
	CGG	CTG	CGG	CGG	AAC	CGG	ccc	GAG (	CTC 1	TTC A	ACC G	GC T	AC C	GC C	CC G	TG	2628
	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	
10			675					680					685			٠	1.4
	CAT	GCC	AGG	GGC	CCC	GCC	GCC	GGG	CAC (	CTG (	STG G	CG T	TC G	AC C	GC G	GC	2676
	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His	Leu	Val	Ala	Phe	Asp	Arg	Gly	•
15		690					695				: '	700					
	GCC	GGG	GGA	GTG	CTG	GCG	CTT	GCC .	ACC (	CGG C	CTC C	CC T	AC G	GG C	rg g	AA	2724
	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Gľu	
20	705					710					715					7,20	
	CAG	TCG	GGC	GGC	TGG	CGG	GAC	ACC (	GCC (	STC (	GAG C	TT G	AA G	CC G	CC A	TG .	2772
	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu	Leu	Glu	Ala	Ala	Met	
25					725	٠.	• •			730					735		
	ACG	GAC	GAA	CTG	ACC	GGC	TCC	ACT '	TTC (	GG (	CG G	GA C	CG G	CG G	CG C	TG	2820
20	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly	Pro	Ala	Ala	Leu	
30				740					745					750		· · .	
	TCA	GAA	GTC	TTC	CGG	GCC	TAC	CCG	GTG (	SCC 1	TG T	TG G	TC C	CC G	CG A	CA :	2868
35	Ser	Glu	Val	Phe	Arg	Ala	Tyr	Pro	Val	Ala	Leu	Leu	Val	Pro	Ala	Thr	·
			755	-	-	'		760					765				
	GGA	GGC	AAG	TCA								;					2880
40	Gly	Gly	Lys	Ser											-		
-		770					•	•									
	TGAC	CGCAC	GCC C	CAACO	SATGO	G GC	CAAC	CCGG	TGC	AGGG	AGC (	GGGG	GCT	rc ga	TAT	C	2936

# SEQ ID NO:11

5	GATCCGGACG	GCAACCTCAT	GTCCCGGAG	GACTGGGACA	GCGGCTTCGG	CCGTTCGGTG.	60
	GGCATGTTCC	TCAACGGCGA	CGGCATCCAG	GGCCACGATG	ACCGCGGCCG	CCGCATCAÇG	120
	GACGTGAACT	TCCTGCTGTA	CTTCAACGCC	CACGACGGCG	ACGTCGAGTT	CACGCTGCCG	180
10	CCGGACGAAT	ACGCCCCGGC	CTGGGACGTC	ATCATCGACA	CCGCCGGTGA	AGGGGCCGAC	240

5	TCC	AAGC	CCG	CGGA	CGCC	GG A	ACCA'	TCCT	G TCC	GTTG	CGG	CCAA	GTCG	CT GO	FTTGT	GCTT	. 300
	CGC	GCCC	ACA	GCGC.	ACCG	GA G	GAGG.	AGCC'	r gac	CATT	CCG	TGGC	TGCT'	TC CC	CTGGC	TĠCA	360
	CTG	ACGC	AGA	CCGC	CACC	GC C	GAGA	CGGC	G GCG	CTCA	CAG	CTCC	TGCC	GT TO	CCGA	.GCCG	420
10	GCC	AAGA	CGA	AGAA	GCCG	GC C	GCTG	ACCC	G GTI	GCTG	AAC (	CGGC	CGAC	CC GC	CGGT	TGCT	480
	GAC	CCGG	CCG	ACCC	GGTT	GC T	GACC	CGGT	r gci	GACC	CGG (	CGCC	GGAA	CC GG	CTGC	GGAG	540
	CCT	GCGA	AAT	CCGC.	AGCG	GA A	CCTG	GTGC	G GAG	CCTG	CGA .	AGGA	CCCG	GA GO	SAGCA	.GCCG	600
15	GCG	GAAA	AGC	CGGC	GCGC.	AA G	CTG	CGGC	A AAG	CGCG	GCG (	GCCA	CCTG	AG GG	CGGT	ÇAAG	660
	ccc	GCTG	GGG	AGGA	CGC												677
	ATG	AGA	ACG	CCA	GTC	TCC	ACG	TAC	AGG	CTG (	CAG A	ATC A	AGG A	AG G	GA T	TC	725
20	Met	Arg	Thr	Pro	Val	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Lys	Gly	Phe	70.7
	1				5			•	٠	10					15	<i>~</i> .	
	ACA	СТС	TTC	GAC	GCG	GCC	AAA	ACC	GTT	CCG 1	rac (	CTG (	CAC T	CG C	TC G	GC	 773
25	Thr	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	•
				20	•		j		25				•	30	•		•
	GTC	GAC	TGG	GTC	TAC	CTT	TCT	CCG	GTC	CTG /	ACT C	SCC C	AG C	AG G	GC T	CC	821
30	Val	Asp	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	
			35					40				, .	45				-
35	GAC	CAC	GGG	TAC	GAC	GTC	ACC	GAT	CCC	TCC_C	SCC C	STC- G	AC C	CC G	AA Č	GC	869
()	Asp	His	Gly	Туг	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	
		50					55		,	• •		60					
40	GGC	GGG	CCG	GAG	GGC	CTC	GCG	GCG	GTT '	TCC A	AG G	CG G	cc c	GC G	CC GC	CG	917
	Gly	Gly	Pro	Glu	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Ala	Ala	
	65					70					75					80	
45	GGC	ATG	GGC	GTG	CTG	ATC	GAC	ATC (	GTG (	CCC A	AC C	CAC	TG G	GC G	TC GC	CG	965
	Gly	Met	Gly	Val	Leu	Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	
					85					90					95	•	
50	ACG	CCG	GCG	CAG	AAC (	ccc ·	TGG '	TGG :	rgg 1	rcg c	TG C	TC A	AG G	AG G	GA CG	C 1	1013
	Thr	Pro	Ala	Gln	Asn	Pro	Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	
				100					105					110			

4.5

155

5	CAG	TCC	CGT	TAC	GCG	GAG	GCG	TTC	GAC (	STC G	AT T	GG G	AC C	TC G	CC GG	G '	1061
	Gln	Ser	Arg	Tyr	Ala	Glu	Ala	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	
			115					120			. · •		125				
10	GGA	CGC	ATC	CGG	CTG	CCG	GTG	CTC	GGC 1	AGC G	AC G	AT G	AC C	TC G	C C	G	1109
	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	
.=		130			`		135		•			140	٠.	•			
15	CTC	GAA	ATC	AGG	GAC	GGG	GAG	CTG	CGG 1	rac 1	'AC G	AC C	AC C	GA T	יכ ככ	G	1157
	Leu	Glu	Ile	Arg	Asp	Gly	Glu	Leu	Arg	Tyr	Tyr	Asp	His	Arg	Phe	Pro	
20	145		•			150	•				155					160	• •
20	CTC	GCC	GAG	GGA	ACC	TAC	GCC	GAA	GGC (	GAC G	CC C	CG C	GG G	AT G	rc ca	C	1205
	Leu	Ala	Glu	Gly	Thr	Туг	Ala	Glu	Gly	Asp	Ala	Pro	Arg	Asp	Val	His	
25					165					170					175		
	GCC	CGG	CAG	CAC	TAC	GAG	CTC	ATC	GGC 1	rGG C	GC C	GC G	CG G	AC AZ	AC GA	(G	1253
	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg	Arg	Ala	Asp	Asn	Glu	
30		· .		180					185			,		190			
	CTG	AAC	TAC	CGC	CGC	TTT	TTC	GCG	GTG 2	AAC A	CG C	TC G	CC G	GC GT	rc co	C	1301
	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu	Ala	Gly	Val	Arg	
35			195			, .	. = .0)	200			• • • •		205				
	GTG	GAA	ATC	CCC	GCC	GTC	TTC	GAC	GAG (	GCA C	CAC C	AG G	AG G	TG G	rg co	C '	1349
	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	Glu	Val	Val	Arg	
40		210					215	•	٠.			220					
	TGG	TTC	CGC	GAG	GAC	CTT	GCG	GAC	GGC (	CTG C	CGG A	TC G	AC C	AC CO	CG GA	VC	1397
	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His	Pro	Asp	•
45	225					230					235	•0			. •	240	/ <u>/</u>
	GGC	CTC	GCT	GAC	ccc	GAG	GGG	TAC	CTG /	AAG C	GA C	TC C	GG G	AA G	C AC	C.	1445
	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val	Thr	
50					245		•	. •		250					255	.•	
										ATC C	,		•				1493
	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln	

5				260					265					27	0	1923	i ş	
	CTG	ccc	GCC	AGC	TTC	GAG	TGT	GAA	GGC	ACC A	ACA	GGC 1	TAC C	GAC	GCC	СТС		1541
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thi	Gly	Туг	As	p Al	a L	eu	
10			275					280					285					
	GCC	GAC	GTC	GAC	CGG	GTT	CTC	GTG	GAC	CCG (	CGC	GGC (	CAG C	SAA	CCG	CTG		1589
	Ala	Asp	Val	Asp	Arg	Val	Leu	Val	Asp	Pro	Arg	, Gly	Gln	Gl	u Pr	o L	eu	
15		290					295	;				300						
	GAC	CGG	CTT	GAC	GCG	TCC	CTG	CGT	GGC (	GGC (	GAG	ccc e	SCC 0	SAC	TAC	CAG		1637
	Asp	Arg	Leu	Asp	Ala	Ser	Leu	. Arg	Gly	Gly	G1u	ı Pro	Ala	As	э Ту	T G	ln	
20	305					310					315	j				3	20	•
•	GAC	ATG	ATC	CGC	GGA	ACC.	AAG	CGC	CGG .	ATC A	ACC (	GAC G	GT A	TC (	CTG	CAC		1685
	Asp	Met	Ile	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	e Le	u H	is	
25					325					330					-33	5 .		
	TCG	GAG	ATC	CTG	CGG	CTG	GC,C	CGG	CTG (	GTT (	CCG	GGC G	AC G	CC .	AAC	GTT		1733
	Ser	Glu	Tle	Leu	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	a As	n V	al	
30				340					345					350	)	5.1		
	TCA	ATC	GAC	GCC	GGA	GCC	GAC	GCT (	CTC	GCC (	GAA A	ATC A	TC G	CC (	GCC	TTC		1781
	Ser	Ile	Asp	Ala	Gly	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Al	a P	he	
<b>35</b>			355					360					365					
	CCG	GTC	TAC	CGC	ACC	TAC	CTG	CCG	GAG (	GGC (	SCC (	GAG G	TC C	TG A	AAG	GAG	:	1829
40	Pro	Val	Tyr	Arg	Thr	Tyr	Leu	Pro	Glu	Gly	Ala	Glu	Val	Let	ı Ly	s G	lu .	
		370					375					380		٠.,				
•	GCG	TGC	GAG	CTT	GCC	GCG	CGT	AGG (	CGG (	ccg (	GAA (	CTC G	AC C	AG (	GCC	ATC	:	1877
45	Ala	Cys	Glu	Leu	Ala	Ala	Arg	Arg	Arg	Pro	Glu	Leu	Asp	Glr	a Al	a I	le	
	385					390				,	395					40	00	
	CAG	GCT	CTG	CAG	CCG	CTG	CTG (	CTG (	GAC A	ACG C	SAC (	CTC G	AG C	TT (	SCC	CGG	:	1925
50	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu	Asp	Thr	Asp	Leu	Glu	Let	ı Al	a Ai	cg	
					405	-				410					41	5		
	CGC	TTC	CAG	CAG	ACC	TCG (	GGC .	ATG (	STC A	ATG G	CC /	AAG G	GC G	TG (	SAG	GAC	:	1973

5	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val	Met	Ala	Lys	Gly	Val	Glu	Asp	
				420					425					430		: .	£**
	ACC	GCG	TTC	TTC	CGC	TAC	AAC	CGC	CTG (	GC A	cc c	TC A	CG G	AA G	rg go	GC .	2021
10	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly	Thr	Leu	Thr	Glu	Val	Gly	
			435					440	٠				445				
	GCC	GAC	ccc	ACC	GAG	TTC	GCC	GTG	GAG (	CCG G	AC G	AG T	TC C	AC G	cc cc	GG	2069
15	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp	Glu	Phe	His	Ala	Arg	
		450					455					460					
	CTG	GCĄ	CGC	CGG	CAG	GCC	GAG	CTT	CCG (	CTG T	CC A	TG A	CG A	CG C	rg ac	GC.	2117
20	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	Met	Thr	Thr	Leu	Ser	
	465					<b>4</b> 70					475					480	
	ACG	CAC	GAC	ACC	AAG	CGC	AGC	GAG	GAC A	ACC C	GA G	CA A	GG A	TT T	CG G	rc	2165
25	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Ser	Val	
					485		• •	;		490					495		
	ATT	TCC	GAG	GTT	GCG	GGT .	GAC	TGG	GAA 2	AAG G	CC T	TG A	AC C	GG C	TG C	GC	2213
30	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg	Leu	Arg	
				500					505					510	_		, F.
	GAC	CTG	GCC	CCG	CTG	CCG	GAC	GGC	CCG (	CŢG Ţ	CC G	CG. C	TG C	TC T	GG C	AG .	2261
35	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp	Gln	
			515					520				,	525				
	GCC	ATT	GCC	GGC	GĆC	TGG	ccc	GCC	AGC (	CGG G	SAA C	GC C	TG C	AG T	AC T	AC	2309
40	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	Tyr	
		530					535			•		540				٠	
4=	GCG	CTG	AAG	GCC	GCG	CGT	GAA	GCG	GGG 2	AAC 1	rcg A	ACC A	AC T	GG A	CC G	AT	2357
45	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	
	545				٠	550			- ,		555					560	
50	CCG	GCC	CCC	GCG	TTC	GAG	GAG	AAG	CTG 2	AAG (	CC C	GCG G	TC G	AC G	CC G	TG	2405
•	Pro	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Аsp	Ala	Val	
					565					570					575		

5	TTC	GAC	AAT	ccc	GCC	GTG	CAG	GCC	GAG (	STG C	AA C	scc c	TC G	TC G	AG C	TC	2453
	Phe	Asp	Asn	Pro	. Ala	, Val	Gln	. Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	
	•			580					585					590			
10	CTG	GAG	CCG	TAC	GGA	GCT	TCG	AAC	TCC (	CTC G	SCC G	CC A	AG, C	TC G	TG C	AG	2501
	Leu	Glu	Pro	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	
			595					600					605				
15	CTG	ACC	ATG	CCC	GGC	GTC	CCG	GAC	GTC 1	rac c	CAG G	GC A	.cg g	AG T	TC T	GG	2549
	Leu	Thr	Met	Pro	Gly	Val	Pro	Asp	Val	Туг	Gln	Gly	Thr	G1u	Phe	Trp	
*		610					615					620		•	Ç	Ş€ +1	
20	GAC	.ccc	TCG	CTG	ACG	GAC.	CCG	GAC.	AAC. C	GG C	ee c	CG T	TCA	GC T	TC. G	AC.	2597
	-Asp.	Arg	Ser	Leu	Thr	Asp	Pro	λsp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	
	625					630					635					640	
25	GAC	CGC	CGC	GCC	GCG	CTG	GAG	CAG	CTG G	SAT G	CC G	GC G	AC C	TT C	CC G	CG	2645
	Asp	Arg	Arg	Ala	Ala	Leu	-Gļu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	
			-		645		٠,			650	٠		• • •		655	•	
30	TCA	TTT	ACC	GAT	GAG	CGG	ACG .	AAG (	CTG C	TA G	TG A	CG T	CG C	GC G	CG CI	rg	2693
	Ser	Phe	Thr	Asp	Glu	Arg	Thr	Lys	Leu	Leu	.Val	Thr	Ser	Arg	Ala	Leu	
35		•		660					665					670			
-	CGG	CTG	CGC	CGG	GAC	CGT	CCG	GAG (	CTG T	TC A	CG G	GG T	AC C	GG C	CG G1	rc	2741
•	Arg	Leu	Arg	Arg	qeA	Arg	Pro	Glu	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	
40			675				•	680				•	685				
	CTG	GCC	AGC	GGG	CCC	GCC (	GCC (	GGG (	CAC C	TĢ Ç	TC G	CG T	TC G	AC CO	SC GG	SC	2789
	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His	Leu	Leu	Ala	Phe	Asp	Arg	Gly	
45		690	÷ :				695					700		· v.	•		
	ACC	GCG	GCG	GCG	CCG	GGT (	GCA 1	rtg <i>p</i>	cc c	TC G	CC A	CG C	GG C	TT CC	CC TA	C :	2837
	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu	Ala	Thr	Arg	Leu	Pro	Tyr	
50	705				•	710					715		-14			720	
	GGG	CTG	GAA	CAG	TCG	GGT (	GGA 1	rgg ç	GG G	AC A	CC G	CC.,G1	rc G/	AA CI	AA T	C	2885
	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu	Leu	Asn	

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735 730 725 ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA 2933 5 Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala 750 745 740 GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG 2981 Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val 755 3002 15 CCG CAG ACA GGA GGA GAG TCA Pro Gln Thr Gly Gly Glu Ser 770 20 TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG 3062 3073 TCTGGGCGCC C The process as claimed in 28, wherein said DNA is derived from a microorganism selected from the group consisting of the genera Rhizobium, Arthrobacter, Brevibacterium, Flavobacterium, Micrococcus, Curtobacterium, Mycobacterium and Terrabacter. 36. The process as claimed in claim 28, wherein said host is a microorganism of the spices Escherichia coli. 30 37. The process as claimed in claim 28, wherein said self-replicable vector is plasmid vector Bluescript II SK(+).

- 38. The process as claimed in claim 28, wherein said transformant is inoculated into a liquid culture medium having a pH of 2-8, and cultured at a temperature of 25-65°C for 1-6 days.
- 39. The process as claimed in claim 28, wherein said recombinant enzyme in the culture is collected by one or more methods selected from the group consisting of centrifugation, filtration, concentration, salting out, dialysis, ion-exchange chromatography, gel filtration chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectrophoresis.
- 40. A method to convert a reducing amylaceous saccharide, which contains a step of allowing the recombinant enzyme of claim 25 to act on a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher to form a non-reducing saccharide having trehalose structure as an end unit from the amylaceous saccharide.
- 41. The method as claimed in claim 40, wherein said recombinant enzyme has the following physicochemical properties:
  - (1) Molecular weight

35

40

45

50

55

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PA-GE); and

- (2) Isoelectric point (pl)
- About 3.6-4.6 on isoelectrophoresis.

42. The m thod as claimed in claim 40, wherein said r combinant enzyme has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

	SEQ	ID 1	10:2		•												
	Met	Arg	Thr	Pro	Ala	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Arg	Gly	Phe	Thr
5	. <b>1</b> .				.5					10					15	e.	
	Leu	Phe	Asp	Ala	Ala	Glu	Thr	Val	Pro	Tyr	Leu	Lys	Ser	Leu	Gly	Val	Asp
			20 ;					25					30				
10	Trp	Ile	Tyr	Leu	Ser	Pro	Ile	Leu	Lys	Ala	Glu	Ser	Gly	Ser	Asp	His	Gly
	35 -		<u>.</u>		eq f	40					45					50	
15			• .														
					•	٠-									•		
20	· i .		7.	• •			•										
	4	2:													,-	*	
		• •											: .			•	
?5		-															

Tyr	Asp	Val	Thr	Ąsp	Pro	Ala	Val	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
		-	55					60					65			
Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	Ala	Arg	Gly	Ala	Gly	Met	Gly	Val	Leu
	70				: <u>.</u>	75					80					85
Ile	Asp	Ile	Val	Pro	Asn	His	Val	Gly	Val	Ala	Ser	Pro	Pro	Gln	Asn	Pro
•				90					95					100		
Trp	Trp	Trp	Ser	Leu	Leu	Lys	Glu	Gly	Arg	Gly	Ser	Pro	Tyr	Ala	Val	Ala
		105					110					115				
Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Ile	Pro	Val	Leu
120					125					130					135	
Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Lys	Asp	Gly	Glu	Leu	Arg
			140					145				:	150			
Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala	Glu	Gly	Ser	Tyr	Arg	Asp	Gly	Asp
	155					160					165			*		1,70
Ser	Pro	Ğln	Asp	Val	His	Gly	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
				175					180					185		
Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Asn	Thr	Leu
		190					195	٠.			-	200	•			
Ala	Gly	Ile	Arg	Val	Glu	Val	Pro	Pro	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
205					210	•		٠		215	,				220	
Val	Val	Arg	Trp	Phe	Arg	Ala	Gly	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
-			225				•	230					235			
Pro	Asp	Gly	Leu	Ala	Дsp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Val
	240			-		245	٠				250					255
Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
<del>.</del> .				260					265					270		
Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
•		275				_	280					285				
Asp	Val		Arg		Phe	Val	qeA	Pro	Arg	Gly	Gln	Val	Pro	Leu	Asp	Arg
	Gly Ile Trp Phe 120 Gly Tyr Ser Arg Ala 205 Val Pro Thr	Gly Leu 70 Ile Asp Trp Trp Phe Asp 120 Gly Ser Tyr Tyr 155 Ser Pro Arg Ala Ala Gly 205 Val Val Pro Asp 240 Thr Gly Leu Pro	Gly Leu Ala 70 Ile Asp Ile Trp Trp Trp 105 Phe Asp Val 120 Gly Ser Asp Tyr Tyr Asp 155 Ser Pro Gln Arg Ala Asp 190 Ala Gly Ile 205 Val Val Arg Pro Asp Gly 240 Thr Gly Gly Leu Pro Ala 275	S5         Gly Leu Ala Ala         70         Ile Asp Ile Val         Trp Trp Trp Ser         105         Phe Asp Val Asp         120         Gly Ser Asp Asp         140         Tyr Tyr Asp His         155         Ser Pro Gln Asp         Arg Ala Asp Asn         190         Ala Gly Ile Arg         205         Val Arg Trp         225         Pro Asp Gly Leu         240         Thr Gly Gly Ala         Leu Pro Ala Ser         275	Gly       Leu       Ala       Ala       Val         70       Fro       Fro       Pro         11e       Asp       Ile       Val       Pro         10e       Trp       Trp       Ser       Leu         105       Fro       Asp       Trp         120       Fro       Asp       Asp       Asp         155       Fro       Asp       Asp       Arg       Inf         Arg       Ala       Asp       Asn       Glu       Inf         Arg       Ala       Arg       Trp       Phe         205       Fro       Asp       Ala       Tyr         Pro       Asp       Ala       Ala       Tyr         Arg       Ala       Arg       Trp       Phe         225       Fro       Ala       Tyr         Arg       Ala       Tyr       Ala       Tyr         Arg       Ala       Ty	Gly       Leu       Ala       Ala       Val       Ser         70	Gly       Leu       Ala       Ala       Val       Ser       Lys         70       75         1le       Asp       Ile       Val       Pro       Asp       His         90       90       105       105       105       105       105       105       105       105       105       105       105       105       105       105       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100        100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100       100<	55         Gly       Leu       Ala       Ala       Val       Ser       Lys       Ala         70	Gly       Leu       Ala       Ala       Val       Ser       Lys       Ala       Ala         Tle       Asp       Ile       Val       Pro       Asp       His       Val       Gly         Trp       Trp       Trp       Ser       Leu       Leu       Lys       Glu       Gly         Phe       Asp       Val       Asp       Leu       Leu       Ala       Gly         120       Trp       Trp       Asp       Trp       Asp       Leu       Ala       Gly         120       Trp       Trp       Asp       Asp       Trp       Leu       Ala       Gly         120       Trp       Trp       Asp       Asp       Ene       Asp       Gln       Leu         120       Trp       Arg       Pro       Ene       Arg       Gln       Leu         121       Trp       Arg       Pro       Ene       Arg       Arg       Pro       Leu       Arg       Gln       Arg       A	55       55       56       41a       Ala       Ala       Ala       Ser       Lys       Ala       Ala       Arg         70	55       55       56         Gly Leu       Ala       Ala       Val       Ser       Lys       Ala       Ala       Arg       Gly         70	G1y       Leu       A1a       A1a       Val       Ser       Lys       A1a       A1a       A7g       G1y       A1a       A7g       G1y       A1a         T1e       Asp       I1e       Val       Pro       Asp       His       Val       G1y       A1a       A1a       Asp       Arg       A	Gly       Leu       Ala       Ala       Val       Ser       Lys       Ala       Ala       Arg       Gly       Ala       Gly       Ala       Gly       Ala       Gly       Ala       Gly       Ala       Ala       Gly       Ala       Ala       Gly       Ala       Ala       Ser       Pro         Trp       Trp       Trp       Ser       Leu       Leu       Lys       Glu       Gly       Ala       Ala       Ser       Pro         Trp       Trp       Ser       Leu       Leu       Lys       Glu       Gly       Arg       Gly       Ser       Pro       Pro         105       Trp       Trp       Asp       Trp       Asp       Leu       Ala       Gly       Arg       Gly       Fro       Pro         120       Trp       Asp       Asp       Asp       Asp       Leu       Ala       Gly       Gly       Arg       Ile       A	G1y         Leu         Ala         Ala         Val         Ser         Lys         Ala         Ala         Ala         Gly         Met           G1y         Asp         11e         Ala         Ala         Val         Fro         Asp         Into         Ala         Ala	G1y         Leu Ala Ala Ala Val Ser Lys Ala Ala Ala Ala Ala Ala Gly Met Gly 70         75         Ser Sy Ala Ala Ala Ala Ala Ala Gly Met Gly 70         75         Ser Sy	Simple   S

5	290			<i>:</i> .		295					300					305	
	Leu	Asp	Ala	Arg	Leu	Arg	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Glu		Met	Ile
				310					315					320			
10	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
		325					330		*:			335					340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Glu	Gln	Thr	Gly	Ile	Pro	Gly	Glu	Ala	Ala
15					345					350					355		
	Ala	Аsp	Ala	Ile	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Ser	Tyr
		•	360	•	•			365					370			3h."	
20	Leu	Pro	Glu	Gly	Ala	Glu	Ile	Leu	Lys.	Glu	Ala	Cys	Asp	Leu		Ala	Arg
	375					380					385					390	
	Arg	Arg	Pro	Glu	Leu	Gly	Gln	Thr	Val	Gln	Leu	Leu	Gln	Pro	Leu	Leu	Leu
25 ·				395					400					405			<b></b>
	Asp	Thr	Asp	Leu	Glu	Ile	Ser	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410	-				415					420					425
30	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
					430					435				_	_440		
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ser	Leu	Glu	Pro	Glu
.35 -		-	445			ý.		450		~ .		•	455				
	Glu	Phe	His	Val	Arg	Met	Ala	Arg	Arg	Gln	λla	Glu	Leu	Pro	Leu	Ser	Met
	460					465					470					475	
40	Thr	Thr	Leu.	Ser	Thr	His	Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg
				480	-		•	4	485					490			
45	Ile	Ser	Val	Ile	Ala	Glu	Val	Ala	Pro	Glu	Trp	Glu	Lys	Ala	Leu	Asp	Arg
~~		495					500					505					510
	Leu	Asn	Thr	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Thr	Leu	Leu	Trp
50				• =	515					520					525		
	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Ser	Туг
			530					535			·		540				

. 35.

5	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Ser	Trp	Thr	Asp	Pro
	545		• *	:		550					555					560	
	Asp	Pro	Ala	Phe	Glu	Glu	Ala	Leu	Ser	Ala	Val	Val	Asp	Ser	Ala	Phe	Asp
10		• ;	*-	565					570				•	575			
	Asn	Pro	Glu	Val	Arg	Ala	Glu	Leu	Glu	Ala	Leu	Val	Gly	Leu	Leu	Ala	Pro
	.~	580		÷.			585					590		٠.	•		595
15	His	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
		•	. •		600					605					610		
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
20	-	;	615	•				620					625			Miles and	
	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Ala	Glu	Arg	Ile	Arg	Ala	Leu
	630	•		•		635					640				5	645	•
25	Asp	Gln	Leu	Asp	Ala	Gly	His	Arg	Pro	Asp	Ser	Phe	Gln	Asp	Glu	Ala	Val
			. •	650			,		655		٠			660		-	
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asn	Arg	Pro	Glu
30		665				,	670					675					680
	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	His	Ala	Arg	Gly	Pro	Ala	Ala	Gly	His
	•	•			685	: .	•			690			-	9	695		
35	Leu	Val	Ala	Phe	Asp	Arg	Gly	Ala	Gly	Gly	Val	Leu	Ala	Leu	Ala	Thr	Arg
			700			•		705					710				
40	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr	Ala	Val	Glu
~	715	•				720		•	•		725			χ.		730	
	Leu	Glu	Ala	Ala	Met	Thr	Asp	Glu	Leu	Thr	Gly	Ser	Thr	Phe	Gly	Pro	Gly
45				735			-		740		٠			745	•		
	Pro	Ala	Ala	Leu	Ser	Glu	Val	Phe	Arg	Ala	·Tyr	Pro	Val	Ala	Leu	Leu	Val
-		750					755					760	•				765
50	Pro	Ala	Thr	Gly	Gly	Lys	Ser					•					
					770							• •					

5	SEQ	ID 1	NO:4														
	Met	Arg	Thr	Pro	Val	Ser	Thr	Tyr	Arg	Leu	Gln	Ile	Arg	Lys	Gly	Phe	Thi
	1				5					10					15		
10	Leu	Phe	Asp	Ala	Ala	Lys	Thr	Val	Pro	Tyr	Leu	His	Ser	Leu	Gly	Val	Ası
			20					25					30				
	Trp	Val	Tyr	Leu	Ser	Pro	Val	Leu	Thr	Ala	Glu	Gln	Gly	Ser	Asp	His	Gl
15	35					40					45				•	50	
	Tyr	Asp	Val	Thr	Asp	Pro	Ser	Ala	Val	Asp	Pro	Glu	Arg	Gly	Gly	Pro	Glu
				55			;		60					65			
20	Gly	Leu	Ala	Ala	Val	Ser	Lys	Ala	.Ala	Arg	Ala	Ala	Gly	Met	Gly	Val	Lev
		70					75					80					85
	Ile	Asp	Ile	Val	Pro	Aśn	His	Val	Gly	Val	Ala	Thr	Pro	Ala	Gln	Asn	Pro
25					90					95	٠				100		
	Trp	Trp	Trp	Ser	Leu	Leu	Ļys	Glu	Gly	Arg	Gln	Ser	Arg	Tyr	Ala	Glu	Ala
			105				`, '*'	110			2- Ş		115				
30 .	Phe	Asp	Val	Asp	Trp	Asp	Leu	Ala	Gly	Gly	Arg	Ile	Arg	Leu	Pro	Val	Leu
•	120					125					130					135	
	Gly	Ser	Asp	Asp	Asp	Leu	Asp	Gln	Leu	Glu	Ile	Arg	Asp	Gly	GIù	Leu	Arg
35	2 0 *	ş		140			-		145					150			
	Tyr	Tyr	Asp	His	Arg	Phe	Pro	Leu	Ala <sup>·</sup>	G1u	Gly	Thr	Tyr	Ala	Glu	Gly	Asp
40		155					160					165					170
40	Ala	Pro	Arg	Asp	Val	His	Ala	Arg	Gln	His	Tyr	Glu	Leu	Ile	Gly	Trp	Arg
-	•				175					180					185		
45	Arg	Ala	Asp	Asn	Glu	Leu	Asn	Tyr	Arg	Arg	Phe	Phe	Ala	Val	Àsn	Thr	Leu
	,	4	190					195	5				200				
	Ala	Gly	Val	Arg	Val	Glu	Ile	Pro	Ala	Val	Phe	Asp	Glu	Ala	His	Gln	Glu
50	205					210					215					220	
	Val	Vạl	Arg	Trp	Phe	Arg	Glu	Asp	Leu	Ala	Asp	Gly	Leu	Arg	Ile	Asp	His
				225					230					235			

_																	
5	Pro	Asp	Gly	Leu	Ala	Asp	Pro	Glu	Gly	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	
		240	•				245					250	•			, Tin	255
	Thr	Gly	Gly	Ala	Tyr	Leu	Leu	Ile	Glu.	Lys	Ile	Leu	Glu	Pro	Gly	Glu	Gln
10					260					265					270		
	Leu	Pro	Ala	Ser	Phe	Glu	Cys	Glu	Gly	Thr	Thr	Gly	Tyr	Asp	Ala	Leu	Ala
15			275					280					285				
	Asp	Val	Asp	Arg	Val	Leu	Val	qsA	Pro	Arg	Gly	Gln	Glu	Pro	Leu	Asp	Arg
	290	·				295					300					305	
20	Leu	Asp	Ala	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Ala	Asp	Tyr	Gln	Asp	Met	Ile
				310	•				315					320		·	
	Arg	Gly	Thr	Lys	Arg	Arg	Ile	Thr	Asp	Gly	Ile	Leu	His	Ser	Glu	Ile	Leu
25	-	325			•		330					335					340
	Arg	Leu	Ala	Arg	Leu	Val	Pro	Gly	Asp	Ala	Asn	Val	Ser	Ile	Asp	Ala	Gly
				e in	345		į			350					355		
30	Ala	Asp	Ala	Leu	Ala	Glu	Ile	Ile	Ala	Ala	Phe	Pro	Val	Tyr	Arg	Thr	Tyr
			360				ē	365	*		•		370	•			
	Leu	Pro	Glu	Gly	Ala	Glu	Val	Leu	Lys	Glu	Ala	Cys	Glu	Leu	Ala	Ala	Arg
35	375					380					385				•	390	
	Arg	Arg	Pro	Glu	Leu	Asp	Gln	Ala	Ile	Gln	Ala	Leu	Gln	Pro	Leu	Leu	Leu
	en s			395					400		**			405			
<del>1</del> 0	Asp	Thr	Asp	Leu	Glu	Leu	Ala	Arg	Arg	Phe	Gln	Gln	Thr	Ser	Gly	Met	Val
		410			٠.		415					420		-			425
	Met	Ala	Lys	Gly	Val	Glu	Asp	Thr	Ala	Phe	Phe	Arg	Tyr	Asn	Arg	Leu	Gly
15					430					435					440		
	Thr	Leu	Thr	Glu	Val	Gly	Ala	Asp	Pro	Thr	Glu	Phe	Ala	Val	Glu	Pro	Asp
		·	445					450					455				•
50	Glu	Phe	His	Ala	Arg	Leu	Ala	Arg	Arg	Gln	Ala	Glu	Leu	Pro	Leu	Ser	
	460					465					470					475	
	Thr	Thr	Leu	Ser	Thr	His	qe <i>k</i>	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg

5				480					485					490			
	Ile	Ser	Val	Ile	Ser	Glu	Val	Ala	Gly	Asp	Trp	Glu	Lys	Ala	Leu	Asn	Arg
40		495					500					505					510
10	Leu	Arg	Asp	Leu	Ala	Pro	Leu	Pro	Asp	Gly	Pro	Leu	Ser	Ala	Leu	Leu	Trp
					515					520					525		
15	Gln	Ala	Ile	Ala	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Gln	Tyr	туг
,,			530			•		535			•		540				
	Ala	Leu	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Asn	Ser	Thr	Asn	Trp	Thr	Asp	Pro
20	545					550			٠.		555					560	
<del>-</del> •	Ala	Pro	Ala	Phe	Glu	Glu	Lys	Leu	Lys	Ala	Ala	Val	Asp	Ala	Val	Phe	Asp
				565					570					575			
25	Asn	Pro	Ala	Val	Gln	Ala	Glu	Val	Glu	Ala	Leu	Val	Glu	Leu	Leu	Glu	Pro
		580					585					590					595
	Tyr	Gly	Ala	Ser	Asn	Ser	Leu	Ala	Ala	Lys	Leu	Val	Gln	Leu	Thr	Met	Pro
30			•		600					605					610	•	
	Gly	Val	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Phe	Trp	Asp	Arg	Ser	Leu	Thr
			615					620					625				:
35	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Phe	Ser	Phe	Asp	Asp	Arg	Arg	Ala	Ala	Leu
	630					635					640					645	
	Glu	Gln	Leu	Asp	Ala	Gly	Asp	Leu	Pro	Ala	Ser	Phe	Thr	Asp	Glu	Arg	Thr
40				650					655					660			
	Lys	Leu	Leu	Val	Thr	Ser	Arg	Ala	Leu	Arg	Leu	Arg	Arg	Asp	Arg	Pro	Glu
		665		4.			670				•	675				•	680
45	Leu	Phe	Thr	Gly	Tyr	Arg	Pro	Val	Leu	Ala	Ser	Gly	Pro	Ala	Ala	Gly	His
				-	685		•			690				٠	695		
	Leu	Leu	Ala	Phe	Asp	Arg	Gly	Thr	Ala	Ala	Ala	Pro	Gly	Ala	Leu	Thr	Leu
50			700					705					710				
	Ala	Thr	Arg	Leu	Pro	Tyr	Gly	Leu	Glu	Gln	Ser	Gly	Gly	Trp	Arg	Asp	Thr
	715					720		4		••• .	725					730	

Ala	Val	Glu	Leu	Asn	Thr	Ala	Met	Lys	Asp	Glu	Leu	Thr	Gly	Ala	Gly	Phe
			735					740					745			
Gly	Pro	Gly	Ala	Val	Lys	Ile	Ala	Asp	Ile	Phe	Arg	Ser	Phe	Pro	Val	Ala
	750		•			755					760					765
Leu					Thr	Gly	Gly	Glu	Ser					• ;	٠	
				770					775						•	

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- 43. The method as claimed in claim 40, wherein said reducing amylaceous saccharide is a member selected from the group consisting of starch hydrolysate and amylaceous substance which has been treated with 15 acid together with or without amylase.
  - 44. The method as claimed in claim 40, wherein said reducing amylaceous saccharide is a member selected from the group consisting of maltotriose, maltotetraose, maltopentaose, maltohexaose, maltohexaose, maltohexaose and mixtures thereof.
  - 45. The method as claimed in claim 40, wherein the reducing amylaceous saccharide is in a solution form with a concentration of 50 w/v % or lower, and the step is carried out at a temperature of 40-55°C and a pH of 5-10.
  - 46. The method as claimed in claim 40, wherein said non-reducing saccharide is a member selected from the group of consisting of  $\alpha$ -glucosyl trehalose,  $\alpha$ -maltosyl trehalose,  $\alpha$ -maltotriosyl trehalose,  $\alpha$ -maltotetraosyl trehalose, α-maltopentaosyl trehalose, and mixtures thereof.

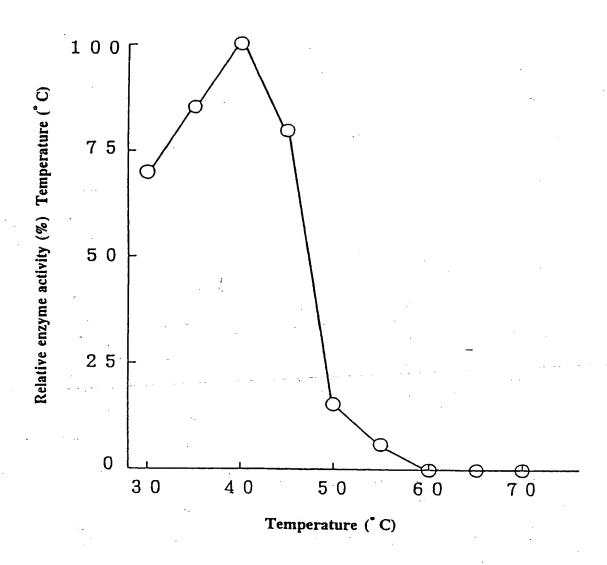


FIG. 1

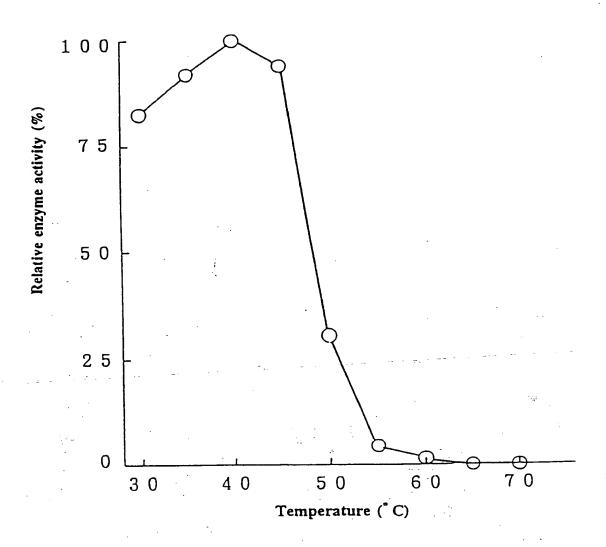


FIG. 2

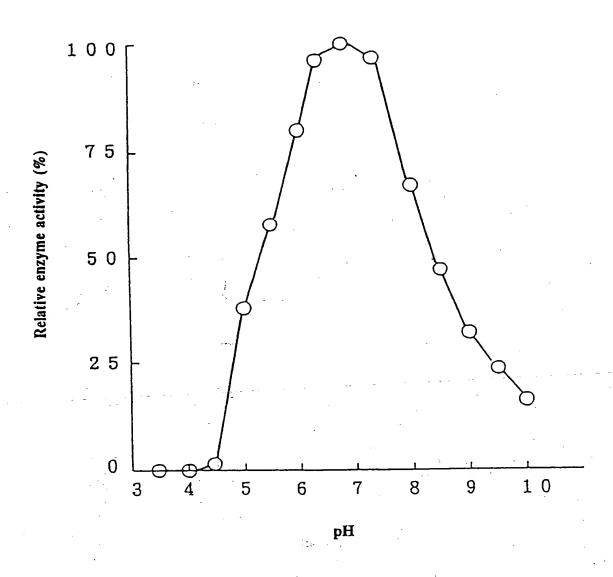
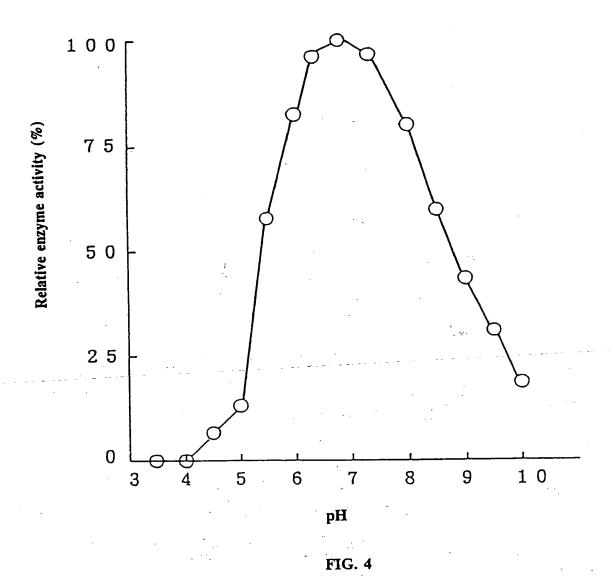


FIG. 3



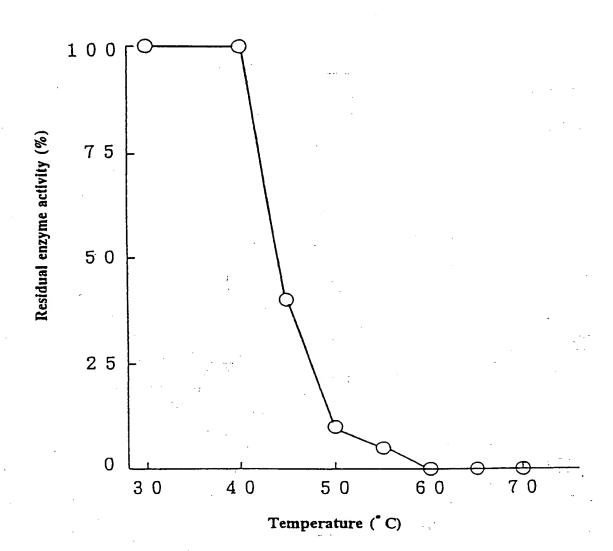


FIG. 5

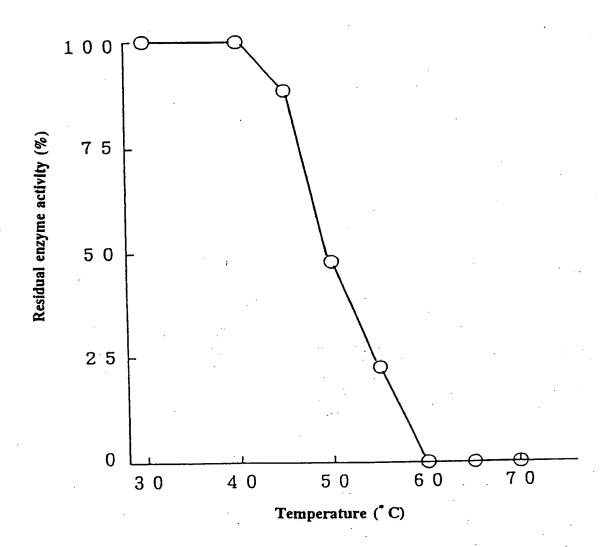


FIG. 6

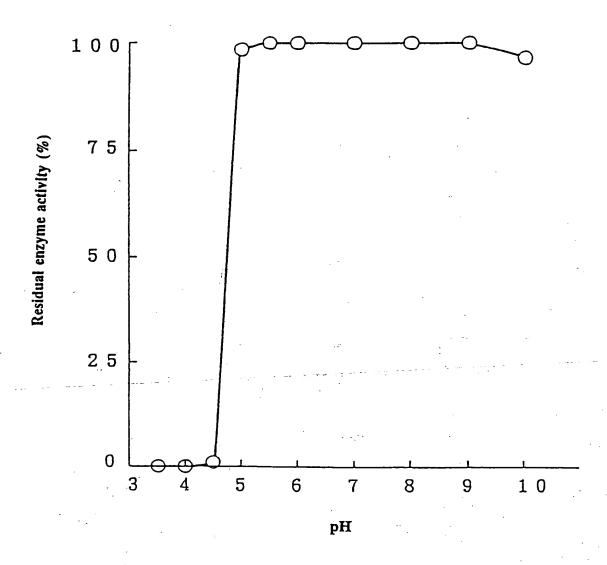


FIG. 7

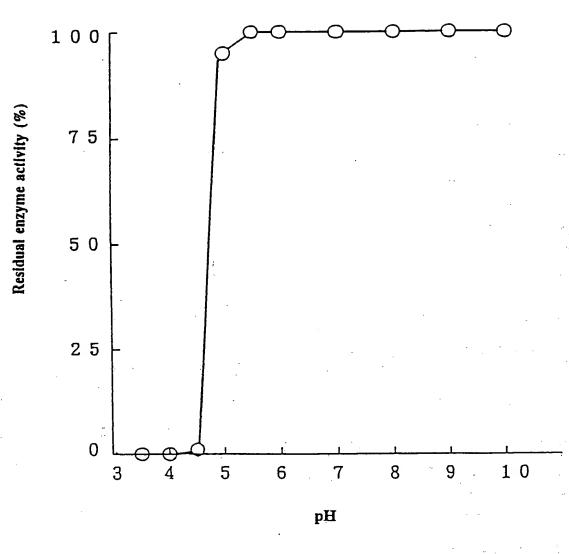


FIG. 8

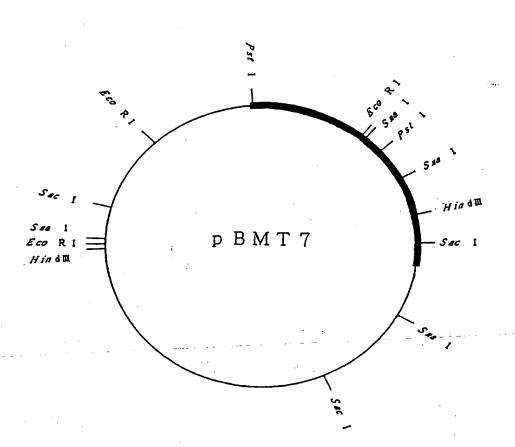


FIG. 9

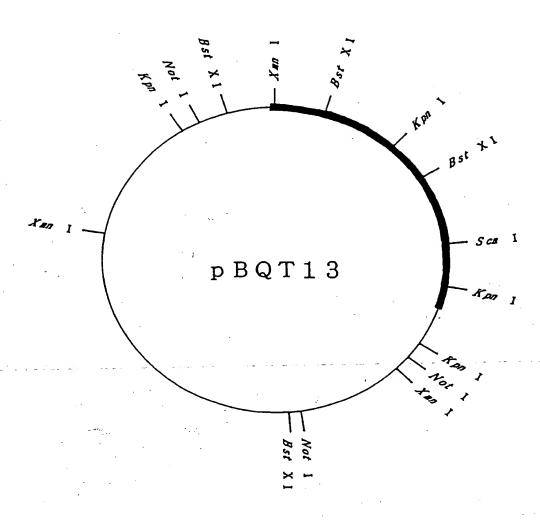


FIG. 10